FIG. 1A

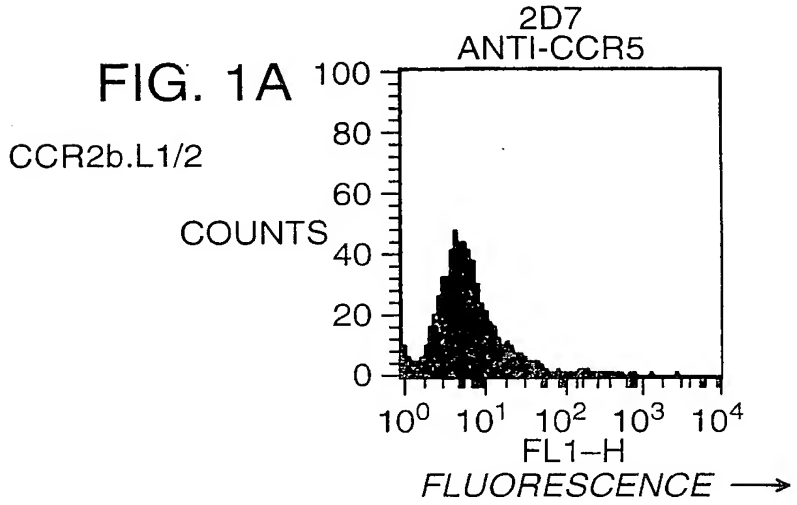


FIG. 1B

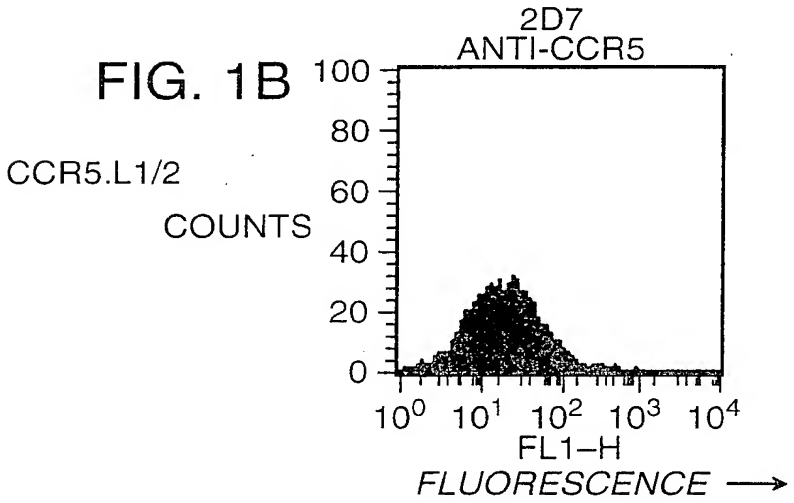
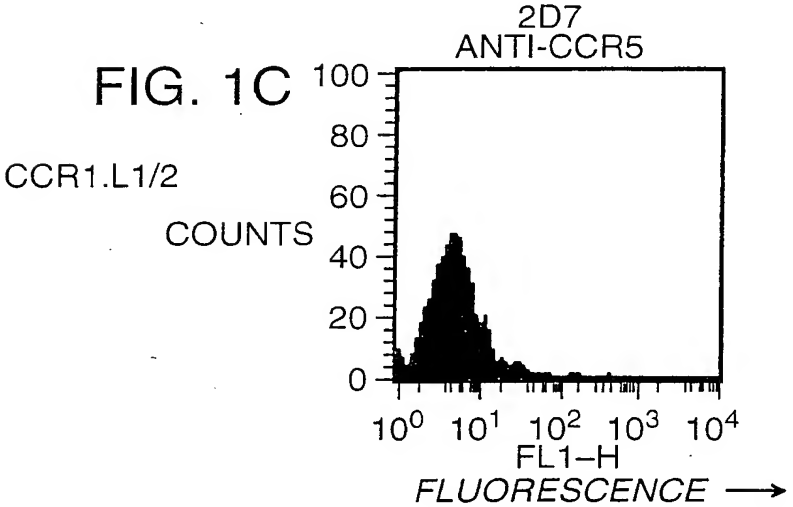


FIG. 1C



BEST AVAILABLE COPY

FIG. 1D

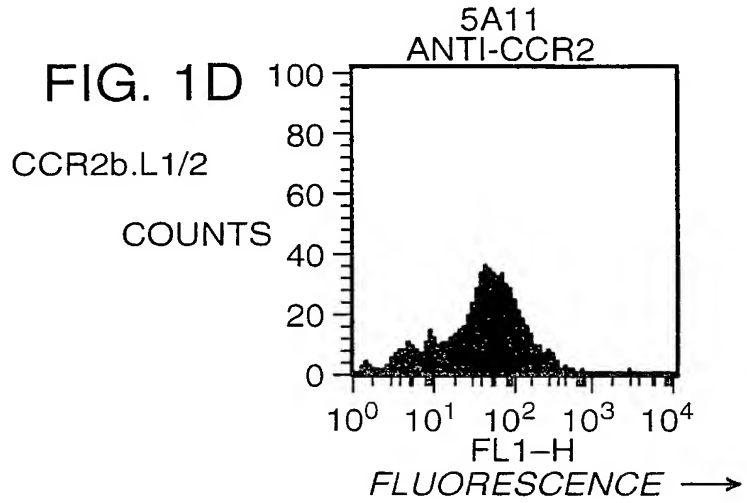


FIG. 1E

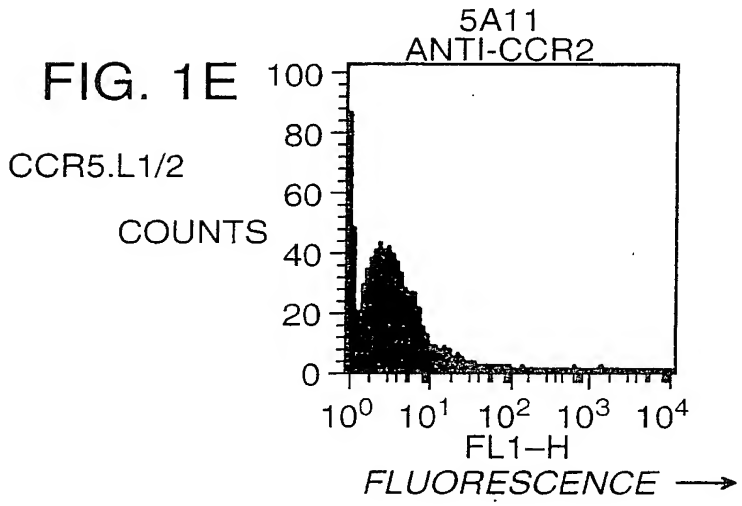
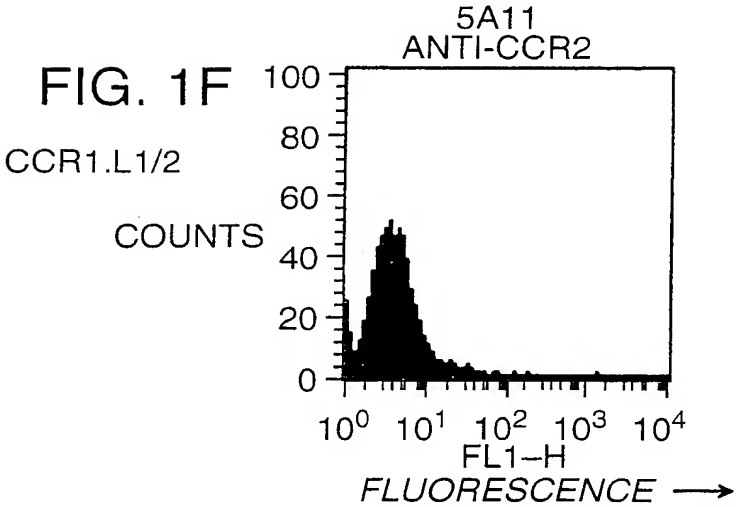


FIG. 1F



BEST AVAILABLE COPY

FIG. 1G

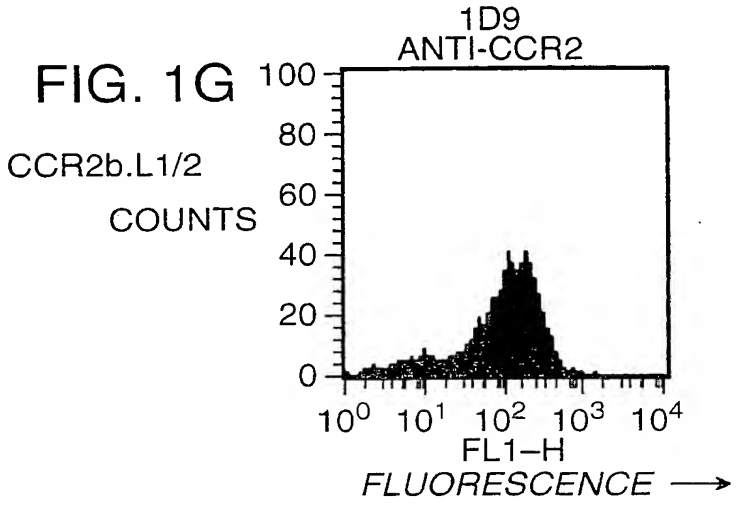


FIG. 1H

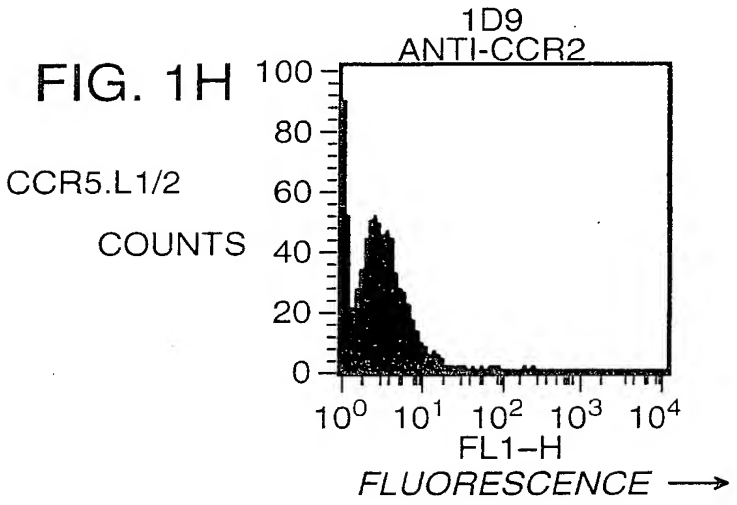
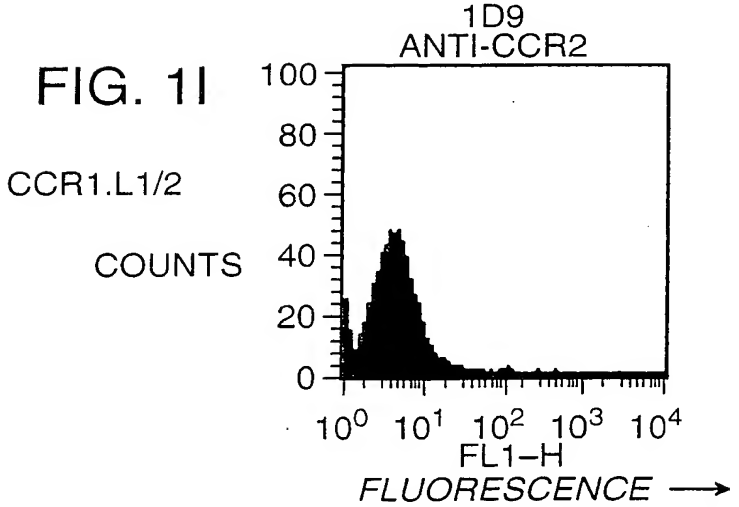


FIG. 1I



BEST AVAILABLE COPY

FIG. 1J

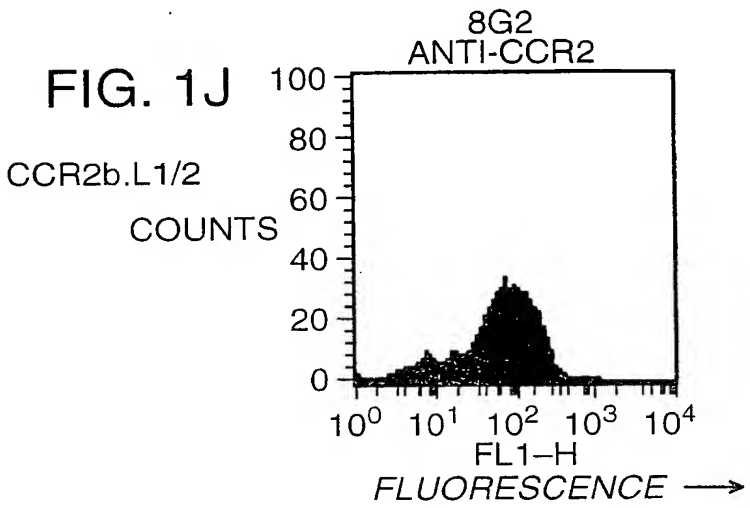


FIG. 1K

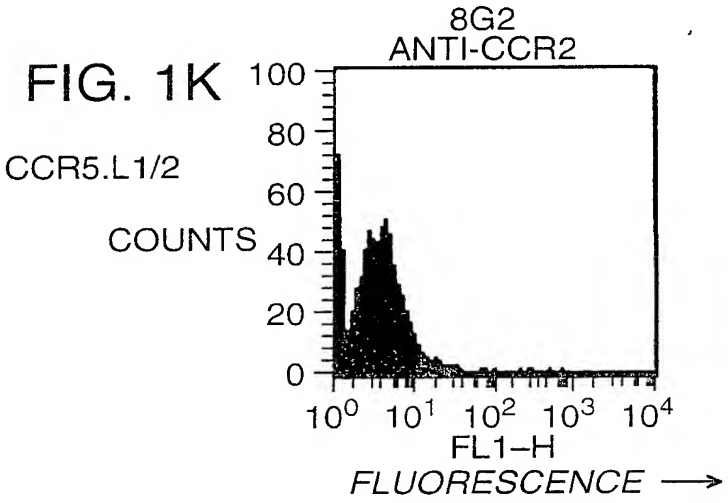
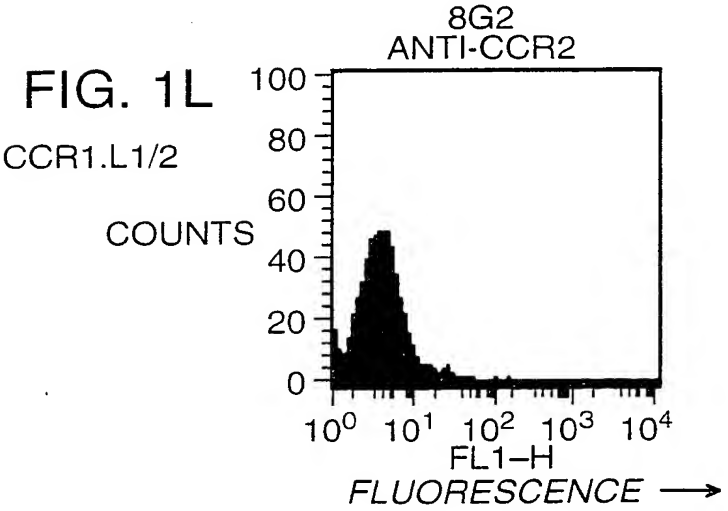


FIG. 1L



BEST AVAILABLE COPY

FIG. 1M

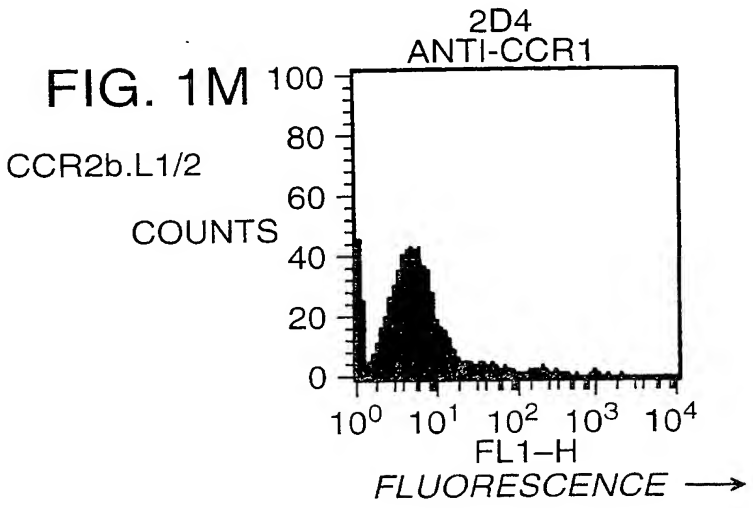


FIG. 1N

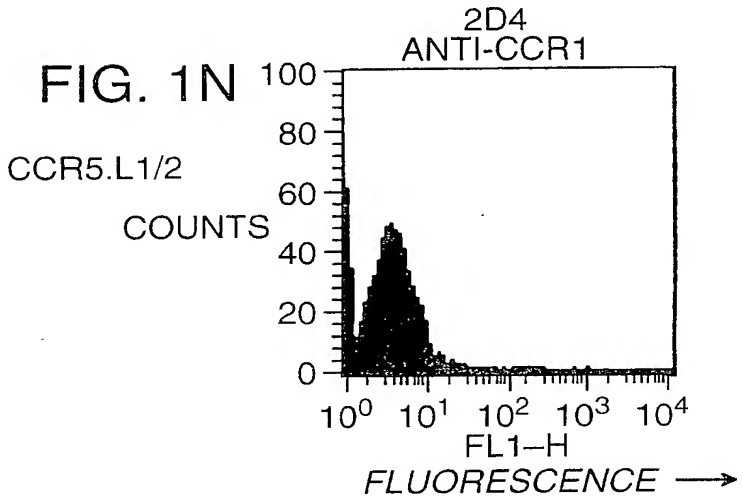
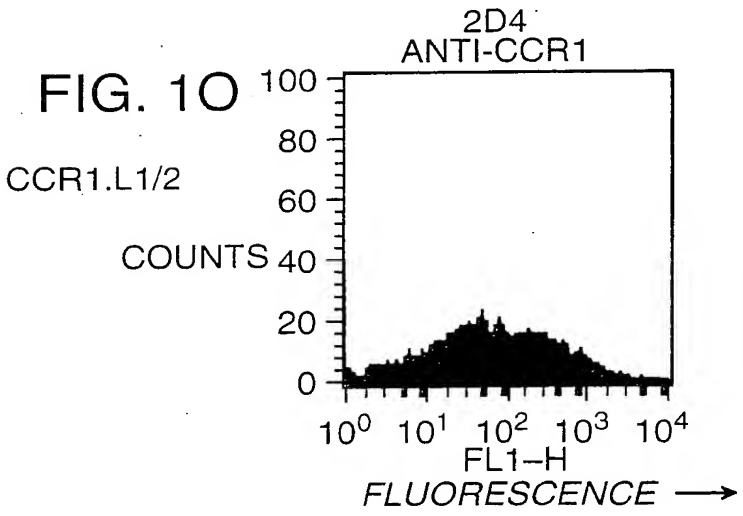


FIG. 1O



BEST AVAILABLE COPY

FIG. 2C

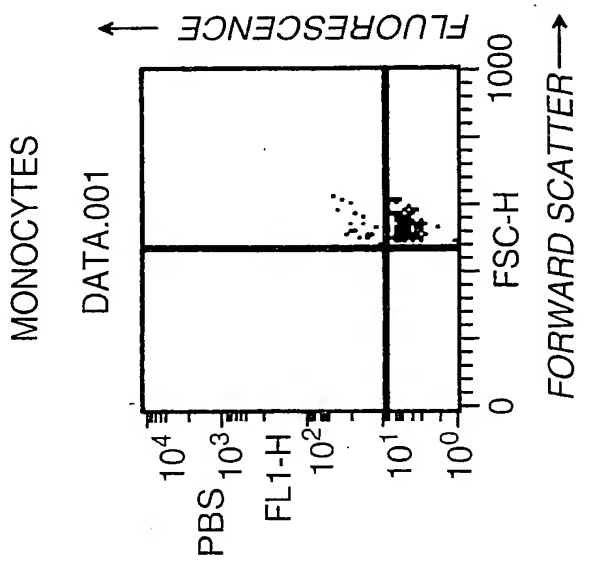


FIG. 2B

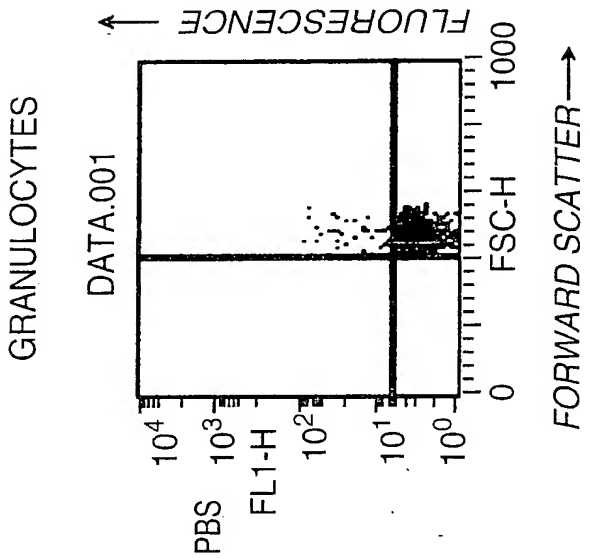
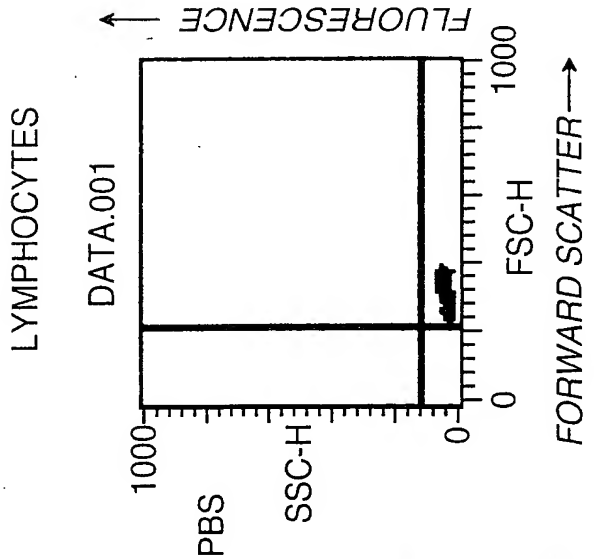


FIG. 2A



BEST AVAILABLE COPY

FIG. 2F

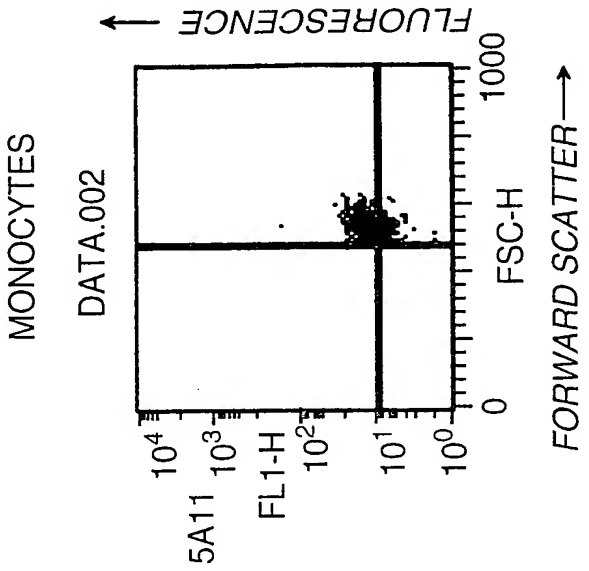


FIG. 2E

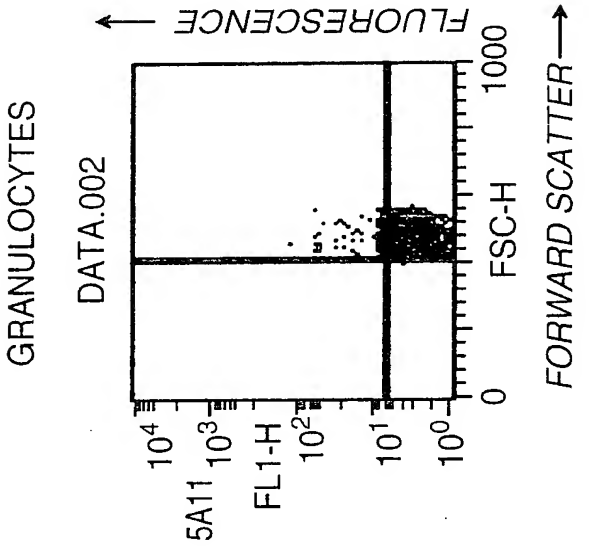
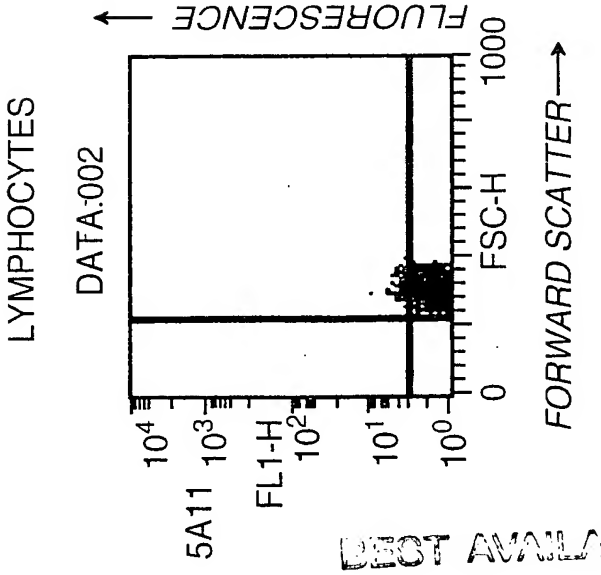


FIG. 2D



BEST AVAILABLE COPY

FIG. 2I

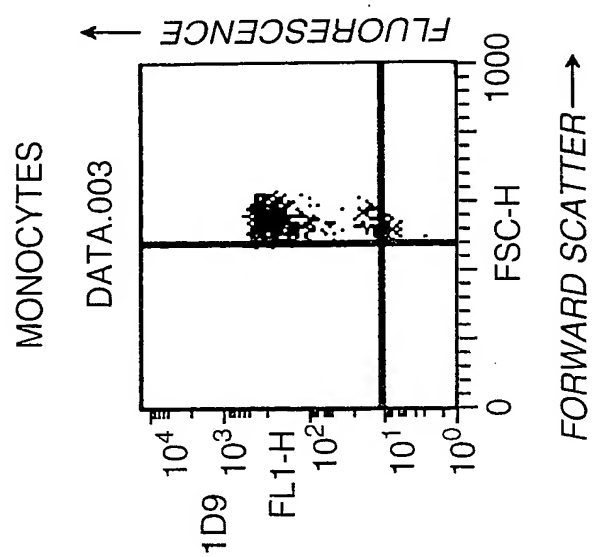


FIG. 2H

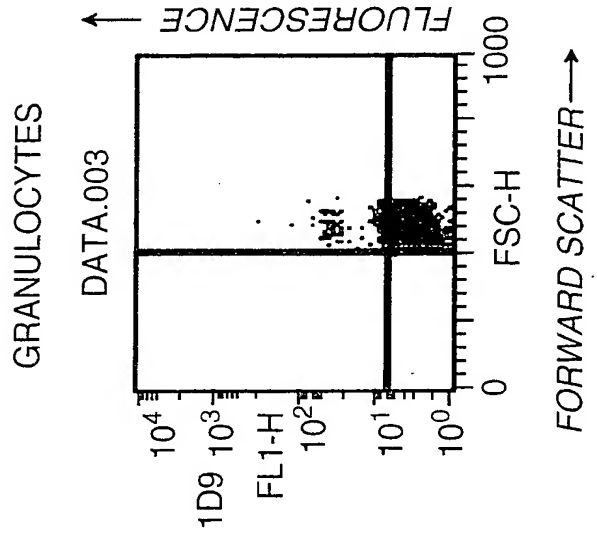
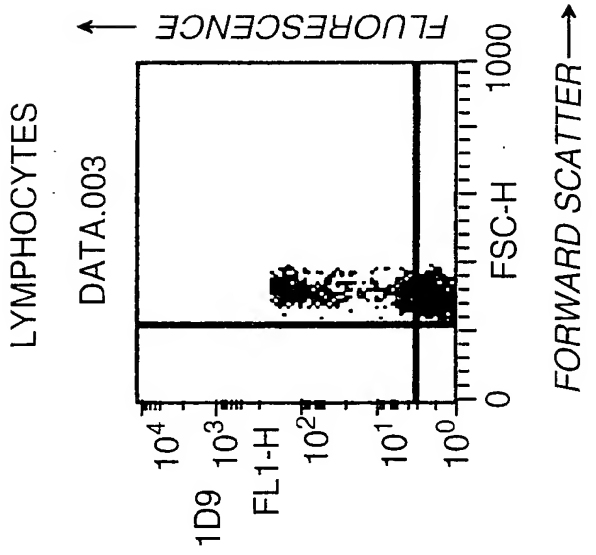


FIG. 2G



NOT AVAILABLE COPY

FIG. 2L

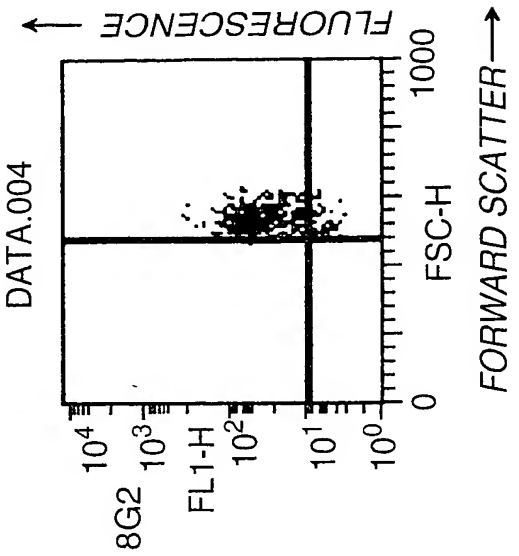


FIG. 2K

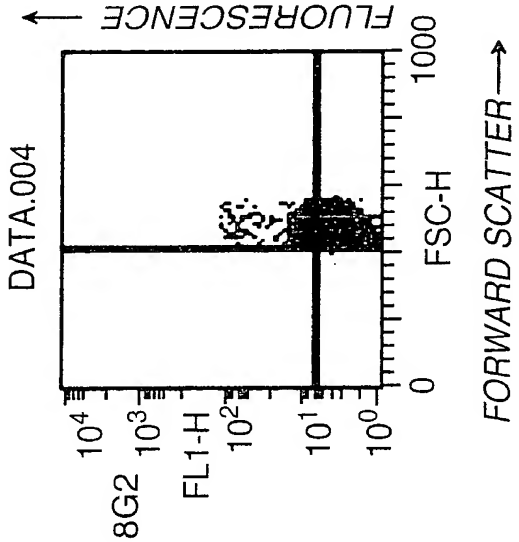
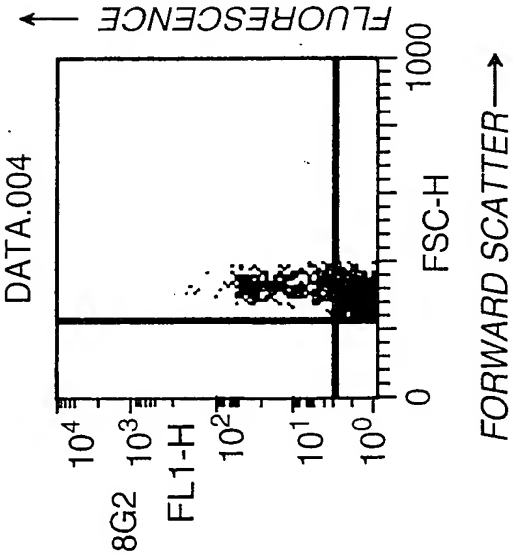


FIG. 2J



BEST AVAILABLE COPY

FIG. 3A

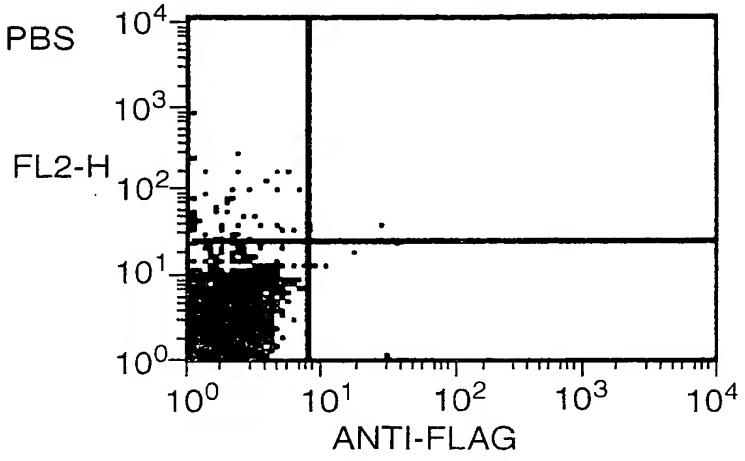


FIG. 3B

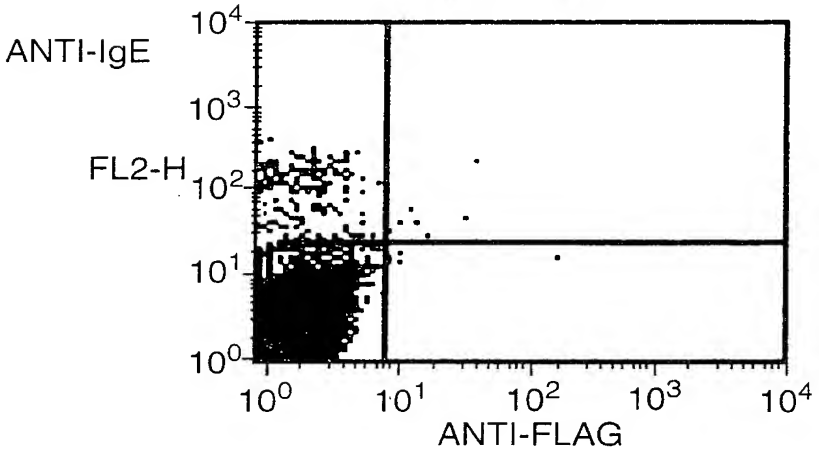
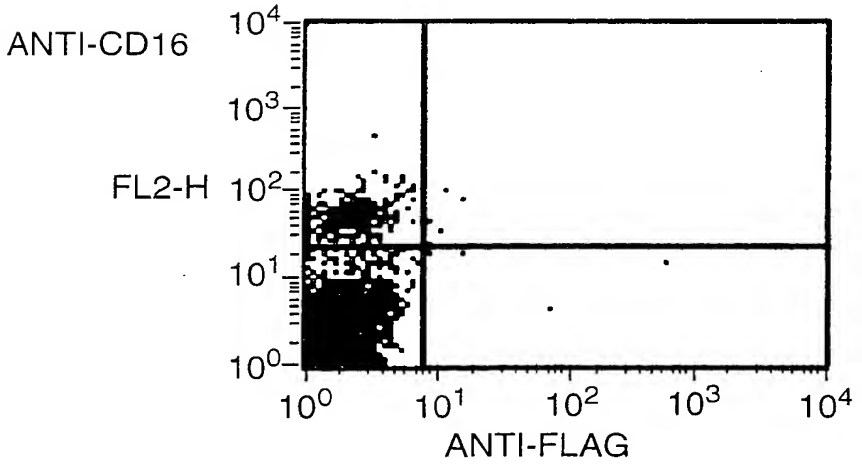


FIG. 3C



BEST AVAILABLE COPY

FIG. 3D

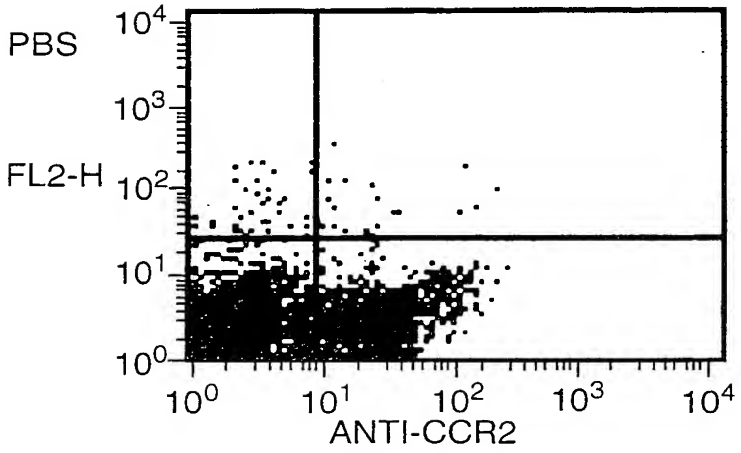


FIG. 3E

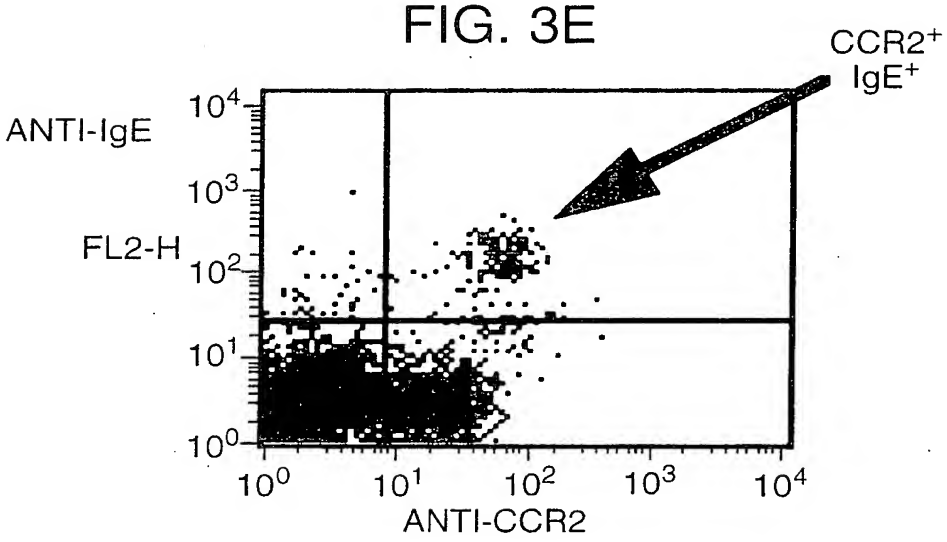
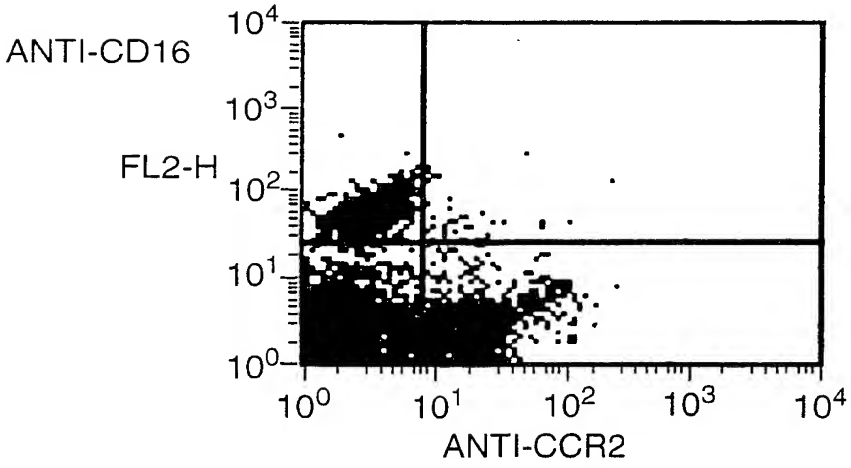


FIG. 3F



BEST AVAILABLE COPY

FIG. 3G

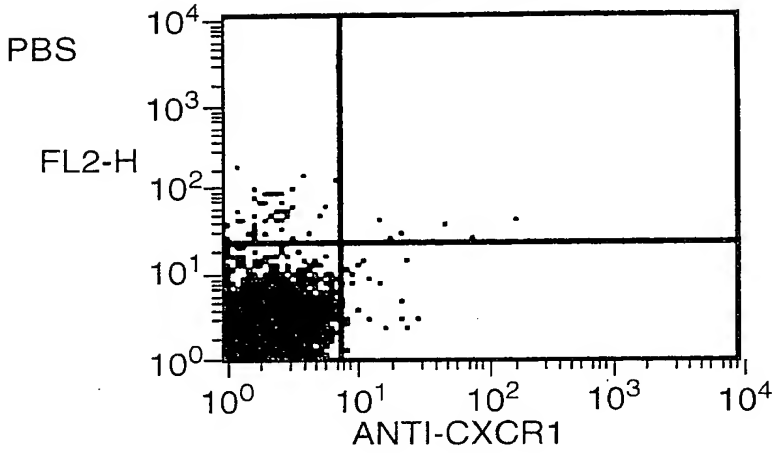


FIG. 3H

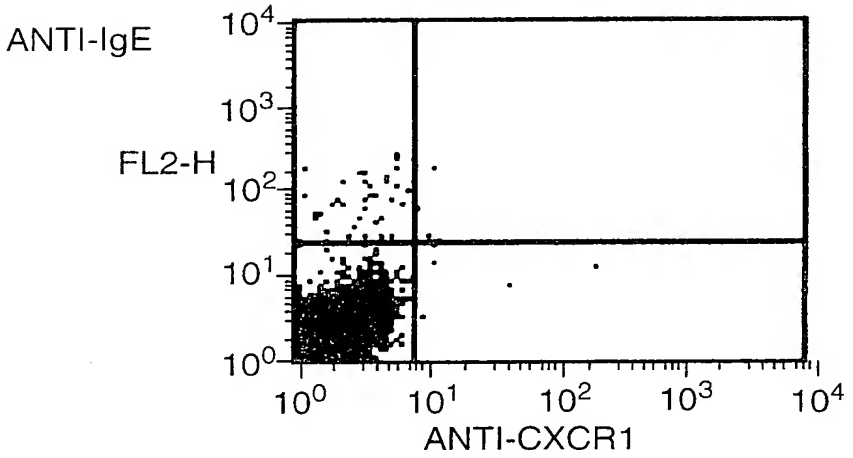
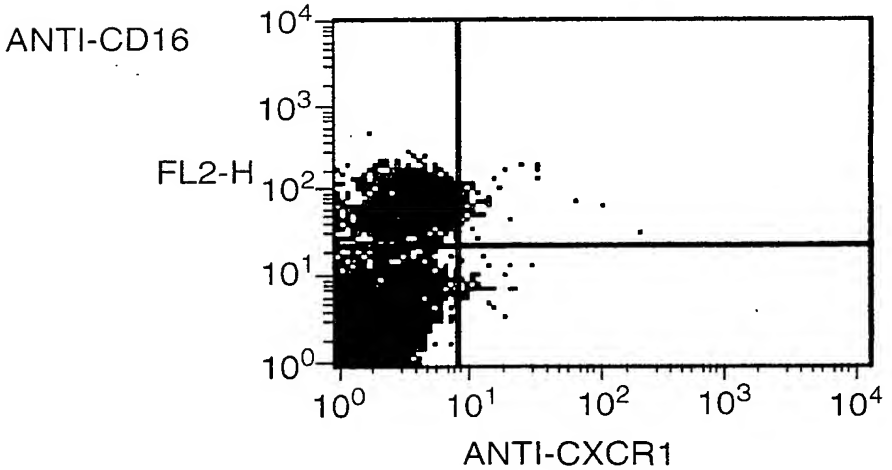
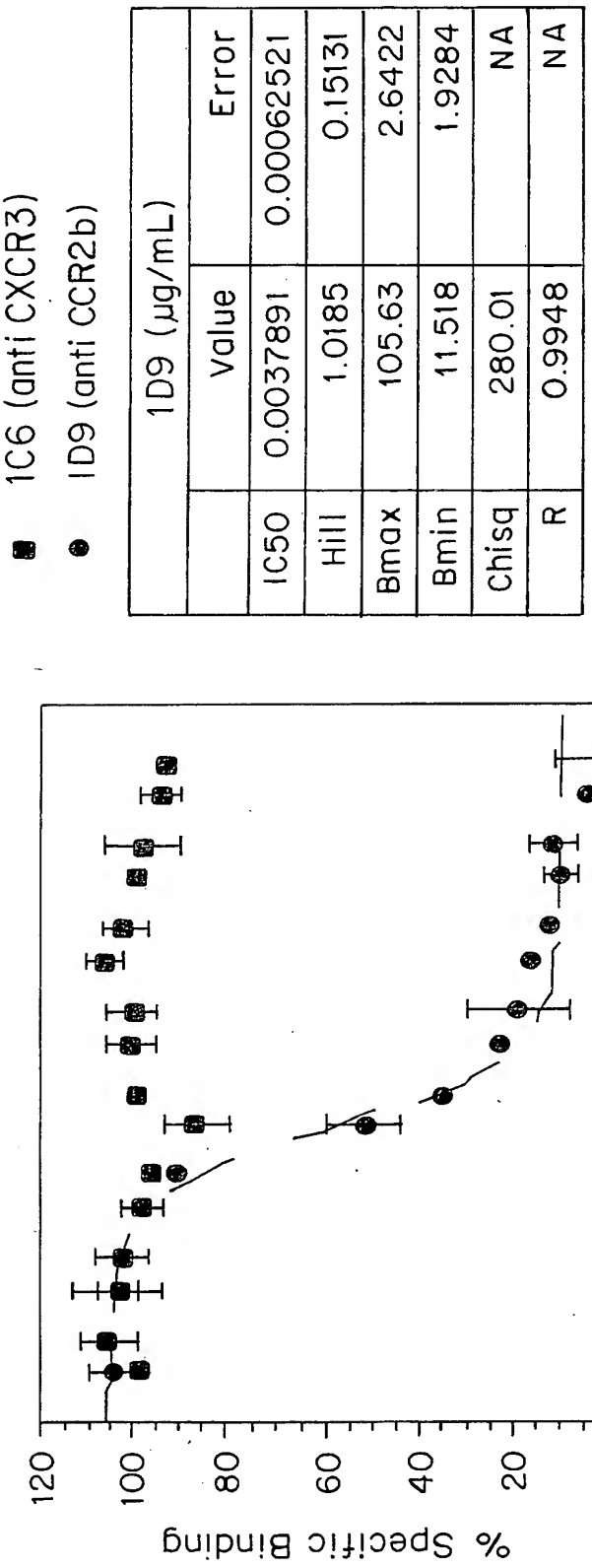


FIG. 3I



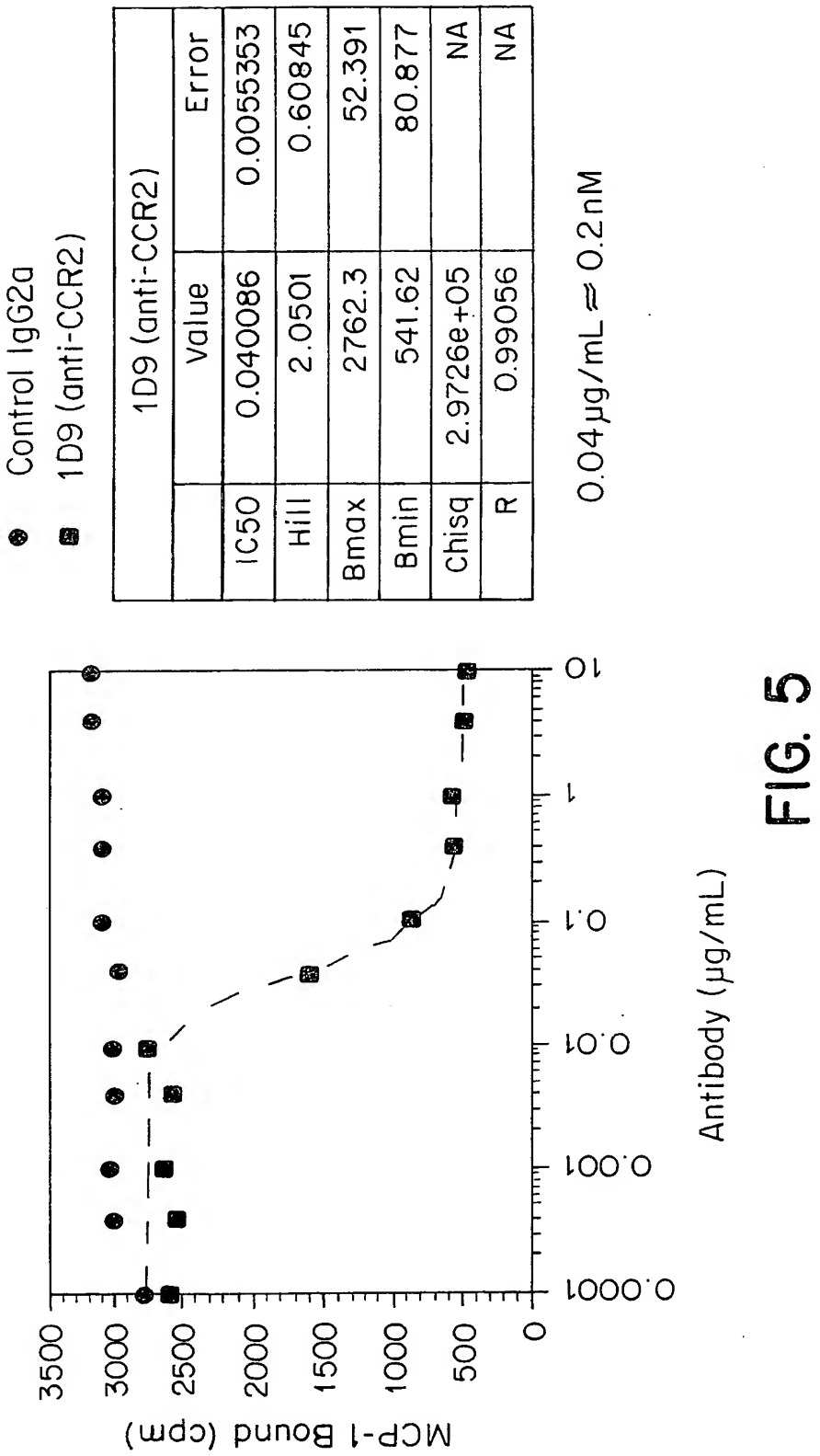
BEST AVAILABLE COPY



1D9 (µg/mL)		
	Value	Error
IC50	0.0037891	0.00062521
Hill	1.0185	0.15131
Bmax	105.63	2.6422
Bmin	11.518	1.9284
Chisq	280.01	NA
R	0.9948	NA

FIG. 4

BEST AVAILABLE COPY



1D9 (anti-CCR2)		
	Value	Error
IC50	0.040086	0.0055353
Hill	2.0501	0.60845
Bmax	2762.3	52.391
Bmin	541.62	80.877
Chisq	2.9726e+05	NA
R	0.99056	NA

FIG. 5

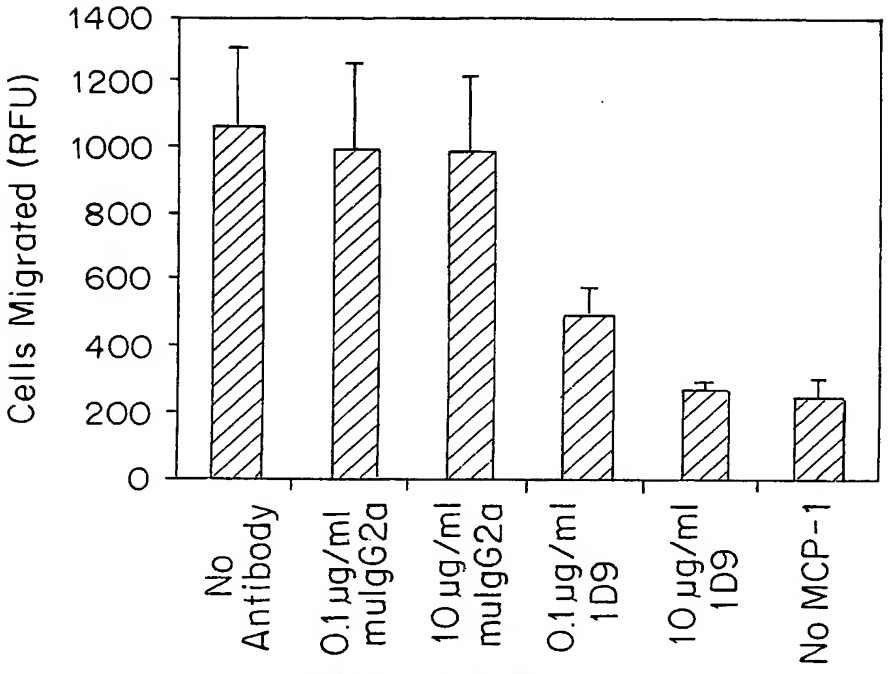

Cells Migrated (RFU)
1400
1200
1000
800
600
400
200
0
No Antibody
0.1 µg/ml mulgG2a
10 µg/ml mulgG2a
0.1 µg/ml 1D9
10 µg/ml 1D9
No MCP-1

FIG. 6A

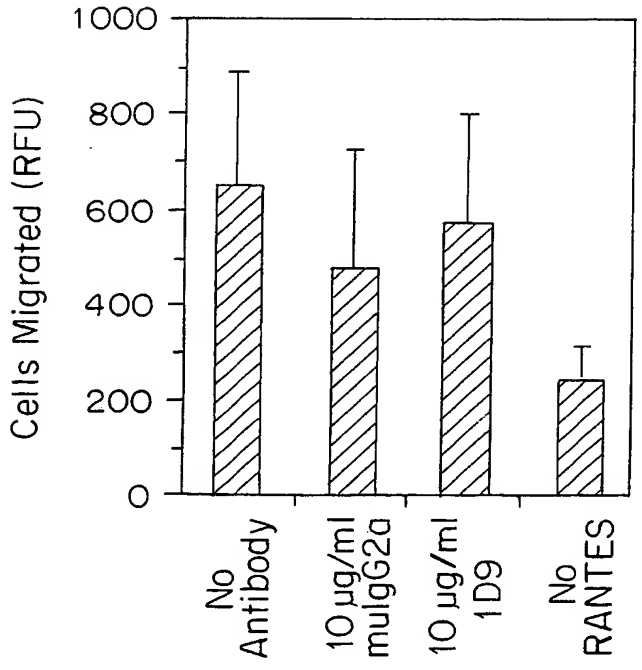

Cells Migrated (RFU)
1000
800
600
400
200
0
No Antibody
10 µg/ml mulgG2a
10 µg/ml 1D9
No RANTES

FIG. 6B

1 DVVMTQTPLT LSVTVGHPAS ISC**KSSQSLL DSDGKTFLN**W LLQRPGQSPK

51 RLIY**LVSKLD S**GVPDRFTGS GSGTDFTLKI SRVEAEDLGV YYC**WQGTHFP**

101 **YT**FGGGTKLE IK

Figure 7

1 EVQLVESGGG LVQPKGSLKL SCAASGFSFN **AYAMN**WVRQA PGKGLEWVA**R**

51 **IRTKNNNYAT YYADSVKD**RY TISRDDSESM LFLQMNNLKT EDTAMYYCVT

101 **FYGNGV**WGTG TTVTVSS

Figure 8

Chothia Canonical Classes

L1 (16 amino acids) = Class 4
Key residues: **2(V)**, 25(SA), 29(L), 33(L), **71(F)**

L2 (7 amino acids) = Class 1
Key residues: **48(IV)**, 51(AT), 52(ST), **64(G)**

L3 (9 amino acids) = Class 1
Key residues: 90(QNH), 95(P)

Martin Canonical Classes

L1 (16 amino acids) = Class 4/16A
Key residues: **2(V), 4(ML), 23(C),** 25(SSP), 26(SN), 27(Q), 29(LI), 30A(HL), 30B(S), 30C(NDS), 30D(G), 32(YS), 33(LF), 34(HEN), **35(W),** 51(V), **71(F), 88(C),** 90(Q), 92(TS), 93(H)

L2 (7 amino acids) = Class 1/7A
Key residues: **23(C)**

L3 (9 amino acids) = Class 1/9A
Key residues: **2(IVL), 3(VQLE), 4(ML),** 28(SNDTE), 30(DYLVISNFGHT), 31(SNTKG), 32(FYNAHSR), 33(MLVIF), **88(C),** 89(QSGFL), 90(QNH), 91(NFGSRDHTYV), 92(NYWTSRQHAD), 93(ENGHTSRAQHAD), 94(DYTVLHNNIWPS), 95(P), 96(PLYRIWF), 97(T), **98(F)**

Figure 9

Chothia Canonical Classes

H1 (5 amino acids) = Class 1
Key residues: **24(AVG), 26(G), 27(FY)**

H2 (19 amino acids) = Class 4
Key residues: 54(S), 55(Y), **71(R)**

Martin Canonical Classes

H1 (5 amino acids) = Class 1/10A
Key residues: **2(VIG), 4(LG), 20(LIMV), 22(C), 24(TAGVS), 26(G), 29(IFLS),** 32(IHYFTNCED), 33(AWGTLV), 34(IVMW), 35(HENQSYT), **36(W), 48(IMLV),** 51(LIVTSN), **69(ILFMV), 78(ALVYF), 80(LM), 90(YF), 92(C), 94(RKGSNH), 102(YHVISDG).**

H2 (19 amino acids) = Class ?/12B
Key residues: **47(W),** 50(RQ), 51(I), 59(Y), **69(I), 71(R), 78(LV)**

Figure 10

```
CDRs                          =======L1========          ==L2===                    ======L3=======

Kabat                  1         2                  3         4         5         6         7         8         9                  10
Numbers   12345678901234567890123456789ABCDEF8901234567890123456789012345678901234567890123456789012345678901234567890123456789ABCDEF67890123456A7

1D9 VK    DVVMTQTPLTLSVTVGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP------YTFGGGTKLEI-K

HF-21/28 VK  ......S..S.P..L.Q......R.....VH. ..N.Y...FQ.......R....K..NR........S..................V.....M....W.       F...Q..R...

1D9RKA VK    DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWFQQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGQGTRLEI-K

1D9RKB VK    DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGQGTRLEI-K

1D9RKC VK    DVVMTQSPLSLPVTLGQPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGGGTRLEI-K

ID9RKD VK    DVVMTQSPLSLPVTLGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP------YTFGGGTRLEI-K
```

Key

1D9 V_K	Mouse 1D9 V_K region
HF-21/28 V_K	Chosen human framework acceptor V_K region sequence with mismatches to the 1D9 V_K region highlighted.
1D9RK$_A$ V_K	CDR grafted 1D9 V_K region, with no back mutations but with the added human lysine residue at position 107 (i.e. 107K).
1D9RK$_B$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L and Q37L, and the additional 107K insertion.
1D9RK$_C$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L, Q37L and Q100G, and the additional 107K insertion.
1D9RK$_D$ V_K	CDR grafted 1D9 V_K region, with back mutations at F36L, Q37L, Q100G and Q17H, and the additional 107K insertion.

Figure 11

```
CDRs                                  ----==H1===              =========H2========                                  ======H3=======

                                                                                                                 1               1
Kabat                 1         2         3         4         5         6         7         8         9         0               1
Numbers   12345678901234567890123456789012345AB67890123456789012ABC34567890123456789012345678901234567890ABC-IJK1234567890123

1D9       EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSESMLFLQMNNLKTEDTAMYYCVTFYGN---------GVWGTGTTVTVSS

4B4'CL V_H ............K.G...R.........T.SNAW.S  ............G..KS.TDGGT.D..AP..G.F.......KNT.Y....S.......V...T.DSLPPH       R...Q..L.....

1D9RH_A V_H EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMN--WVRQAPGKGLEWVGRIRTKNNNYATYYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RH_B V_H EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVGRIRTKNNNYATYYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RH_C V_H EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGN---------GVWGQGTLVTVSS

1D9RH_D V_H EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSKNTLYLQMNSLKTEDTAVYYCVTFYGN---------GVWGQGTLVTVSS
```

Key

1D9 V_H	Mouse 1D9 V_H region.
4B4'CL V_H	Chosen human framework acceptor V_H region sequence with mismatches to the 1D9 V_H region highlighted.
1D9RH$_A$ V_H	CDR grafted 1D9 V_H region, with no back mutations.
1D9RH$_B$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S and S30N.
1D9RH$_C$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S, S30N, G49A and F67Y.
1D9RH$_D$ V_H	CDR grafted 1D9 V_H region, with back mutations at T28S, S30N, G49A, F67Y and T93V.

Figure 12

Sequence Name	Identical Residues	Amino Acid Sequence
1D9 V_K	114	DVVMTQTPLTLSVTVGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP
70/3	97	.....I.Q.....Y.....
70/1	94	.....I.Q.....Y. N...Y.....V.....
70/2	82	.....XLHS....I.Q.....Y. N...Y.....V.P.....Y.....S.....XP.....X.M.D....
V-IB	76	.....S.P.SL.DQ.....R.....VH. N.N.Y.Y.Y..K.....L...R..NRF.....S.....F.F....V.
V-1C	75	.....S.P.SL.DQ.....R....IVH. N.N.Y.E.Y..K.....L...K..NRL.....S.....F..S.V.
V-1A/K5.1/K5.1	75	.....S.P.SL.DQ.....R.....VH. N.N.Y.H.Y..K.....L...K..NRF.....S.....F.S.S..V.
V-1C/V1A5/K1A5	74	..L.....S.P.SL.DQ.....R....IVH. N.N.Y.E.Y..K.....L...K..NRF.....S.....F..S.V.
K18.1	73	.A.....S.P.SL.DQ.....R.....EN. N.N.Y...Y..K.....QL...R..NRF...L...S.....F.L.V..V.
1F	71	..LL.....F.P.SL.DQ.....S.....VH. N.NYY.E.H..KS...LQL...E...RH.....S.....P.....F....L.
24A	68	.I....AAFSNP..L.TS.....R..K...H. S.N.Y.Y.F..K.....QL...YI.N.A.....S.....R.....V.....M..LEY.
167/24	67	.I.I..DE.SNP..S.ESV....R..K...YK ....Y...F.....QL....M.TRA...S...S.....E....K...V.....Q.LVEY.
24B	66	.I....AAFSNP..L.TS....R..K...H. N.I.Y.Y.Y..K.....QL...QM.N.A.....SS.....R.....V.....A.NLEL.

Figure 13

Sequence Name	Identical Residues	Amino Acid Sequence
1D9 V_H	117	EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTISRDDSESMLFLQMNNLKTEDTAMYYCVTF
MRL-RF24BG	86	......VWWRM.....T..T.... .....S.SS.....F.....Q...Y.....I-
V(H)22.1	70	..K.E.....G..M....V....T.SN.W.S ....S.E.....Q..L.SD....H..E...G.F.....K.SVY.....RA...GI...TG-
V11/pBV19B4	66	..K.....G...R....T...T.TD.Y.S ....P...A...LGF..N.A.G.T.E.SA...G.F.....N.Q.I.Y....T.RA..S.T...AR-
Vh7183(Vh69.1)	66	..K.....K.G.....T.SS.T.S ....S.E.R.....T.SS--GGSY...P....G.F.....NAKNT.Y...SS..S.....TR-
VH10-19	65	D.K.....K.G.....T.SS.T.S ....T.E.R.....T.SS--GGSY...P....G.F.....NAKNT.Y...SS..S.....TR-
VHE4-psi	65	.L.....G..R.....T.SS...S ....T.E.R.....A.S.--DGSFI.XP.T..G.F.....NAKNT.....SS.RY.....LR-
V(H)50.1	65	..K.....G.....T...T.SD.Y.Y ....T.E.R.....Y.SN--GGGS...P.T..G.F.....NAKNT.Y...SR..S.....AR-
V3	65	..K.....GA..R....S...T.TD.Y.. ..HRP...P...L.L..N.A.G.I.E.SA.M.G.F.....N.Q.I.Y....T.S...S.T...ARD
V1/pBV132	64	..K.....G...R....T...T.SDFY.E ....P...R...I.AS.N.A.D.T.E.SA...G.FIV...T.Q.I.Y....A.RA....I...AR-
VH283	64	..M.....K.G.....T.SS.T.S ....T.E.R.....T.SS--GGGN...P....G.F.....NAKNN.Y...SS.RS....L...AR-
V(H)37.1	63	..K.....K.G.....T...T.SS.G.S ....T.E.R.....T.SG--GGSY...P....G.F.....NAKNN.Y...SS.RS....L...AR-
V13	61	..K.M.....GA..R...E....T.TD.Y.S ....L.R.SP..L.L..N.A.G.T.E.SA...G.F.....N.QNI.Y....T.RA.AS.T...AKD
V-H_441/V441	59	..K.L.....G.....D.SR.W.S .....IGE.NP--DSSTIN.TP.L..KFI....NAKNT.Y...SKVRS....L...AR-
68-5N	59	---------.....G.....T.SS.G.S ....T.D.R..L..T.NS--.GGS...P....G.F.....NAKNT.Y...SS..S.....AR-
76-1BG/VH7183.9	58	---------...K.G.....T.SS...S ....T.E.R.....T.SS--GGSY...P....G.F.....NAKNT.Y...SS.RS.....AR-
61-1P	58	---------.....G..R.....T.SSFG.H ......E.....Y.SS--GSSTI....T..G.F.....NPKNT.....TS.RS.....AR-
57-1M/VH7183.12	58	---------...K.G.....T.SS...S ....T.E.R.....S.S---SGGS...P....G.F.....NARNI.Y...SS.RS.....AR-
V(H)55	56	..K.L.....G...N.....D.SR.W.S .A.....Q..IGE.NP--GSSTIN.TP.L..KFI....NAKNT.Y...SKVRS....L...AR-
VH7183.13	55	----------.K.G.....T.SS.T.S ....T.E.R.....Y.SN--GGGS...P.T..G.F.....NAKNT.Y...SS..S.....AR-

Figure 14

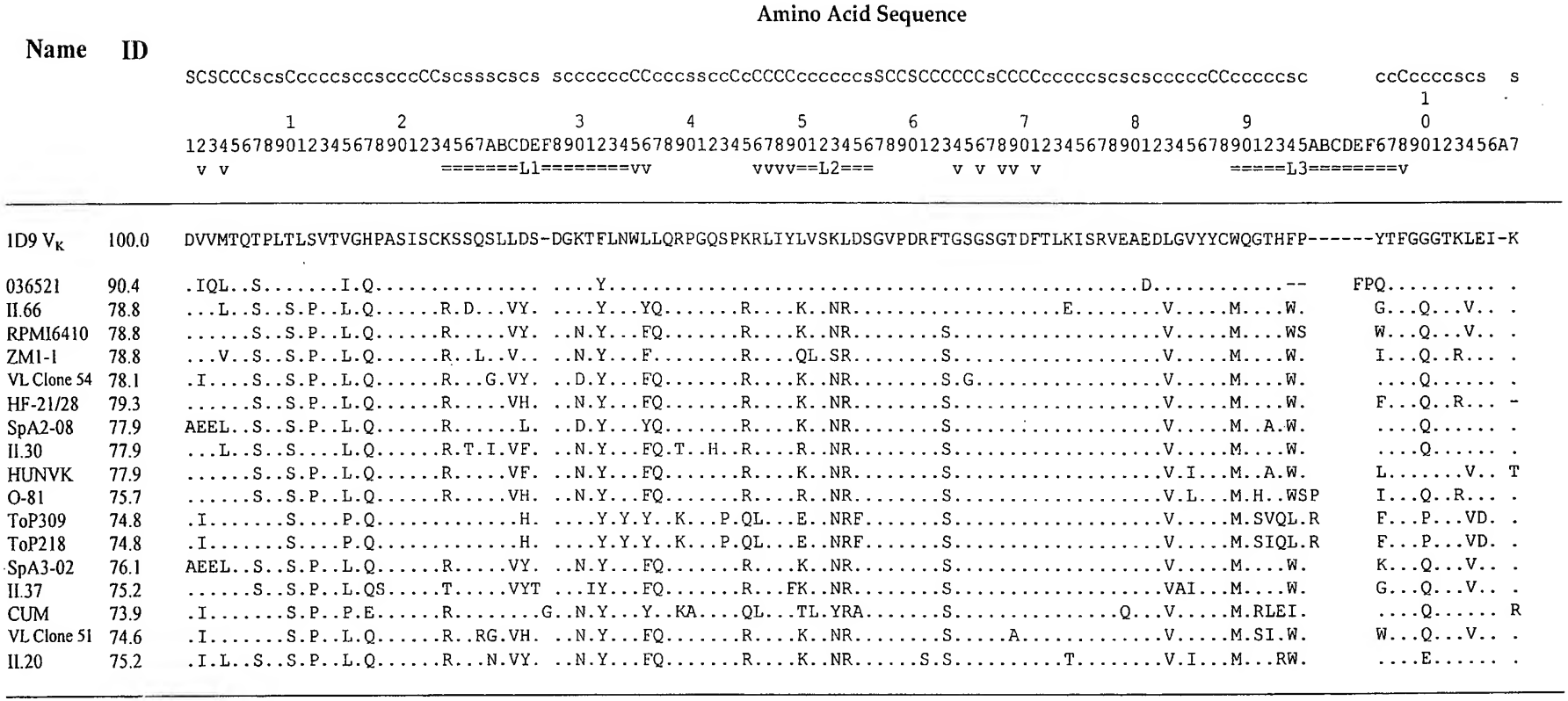

Amino Acid Sequence
Name
ID
1D9 V_K 100.0 DVVMTQTPLTLSVTVGHPASISCKSSQSLLDS-DGKTFLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP------YTFGGGTKLEI-K
036521 90.4
II.66 78.8
RPMI6410 78.8
ZM1-1 78.8
VL Clone 54 78.1
HF-21/28 79.3
SpA2-08 77.9
II.30 77.9
HUNVK 77.9
O-81 75.7
ToP309 74.8
ToP218 74.8
SpA3-02 76.1
II.37 75.2
CUM 73.9
VL Clone 51 74.6
II.20 75.2

Figure 15

Name	ID	Surface	Core	Kabat CDR	FR	FR Surface	Core FR	FR Near CDR	Vernier	V_K	J Chain	Closest Human Germline Gene	L1 Len	L2 Len	L3 Len	L1 Class	L2 Class	L3 Class
1D9 V_K	100.0	30	82	32	82	22	60	33	14	100	14		16	7	9	4	1	1
036521	90.4	27	76	28	75	19	56	31	13	90	13	DPK19-A1+						
II.66	78.8	25	67	22	69	18	52	30	13	80	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
RPMI6410	78.8	25	67	22	69	18	52	30	13	79	12	DPK18-A17+	Same	Same	Same	Same	Same	?
ZM1-1	78.8	25	66	21	68	18	52	30	13	79	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
VL clone 54	78.1	25	66	21	68	18	52	30	13	79	12	DPK18-A17+	Same	Same	Same	?	Same	Same
HF-21/28	79.3	24	66	21	68	18	52	30	13	78	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
SpA2-08	77.9	24	65	21	68	18	51	30	13	77	12	DPK18-A17+	Same	Same	Same	?	Same	Same
II.30	77.9	24	65	21	68	18	51	30	12	77	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
HUNVK	77.9	24	65	21	68	18	51	30	12	77	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
O-81	75.7	24	65	21	68	18	51	30	12	77	12	DPK18-A17+	Same	Same	10	Same	Same	?
ToP309	74.8	24	64	20	68	18	51	29	12	76	12	DPK12-A2+	Same	Same	10	?	Same	?
ToP218	74.8	24	64	20	68	18	51	29	12	76	12	DPK12-A2+	Same	Same	10	?	Same	?
SpA3-02	76.1	24	63	20	68	18	51	29	12	76	12	DPK18-A17+	Same	Same	Same	?	Same	Same
II.37	75.2	24	63	20	68	18	51	29	12	76	12	DPK18-A17+	Same	Same	Same	Same	Same	Same
CUM	73.9	24	63	20	68	18	50	29	12	75	12	DPK36-Chr22 4	17	Same	Same	3	Same	Same
VL clone 51	74.6	24	62	20	67	18	50	29	12	75	12	DPK18-A17+	Same	Same	Same	?	Same	Same
II.20	75.2	23	62	20	67	18	50	29	12	75	12	DPK18-A17+	Same	Same	Same	?	Same	Same

Figure 16

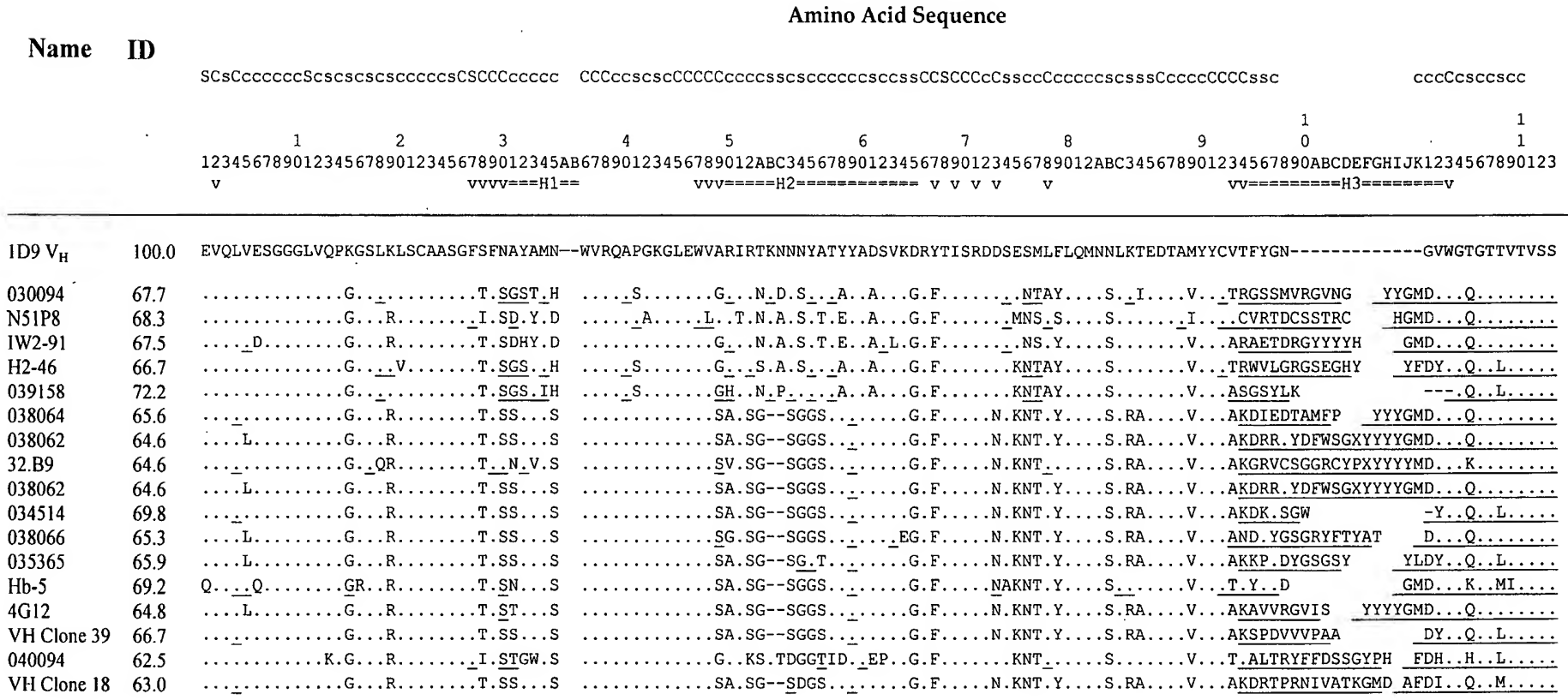

Amino Acid Sequence
Name
ID
1D9 V_H 100.0
030094 67.7
N51P8 68.3
1W2-91 67.5
H2-46 66.7
039158 72.2
038064 65.6
038062 64.6
32.B9 64.6
038062 64.6
034514 69.8
038066 65.3
035365 65.9
Hb-5 69.2
4G12 64.8
VH Clone 39 66.7
040094 62.5
VH Clone 18 63.0

Figure 17A

Amino Acid Sequence

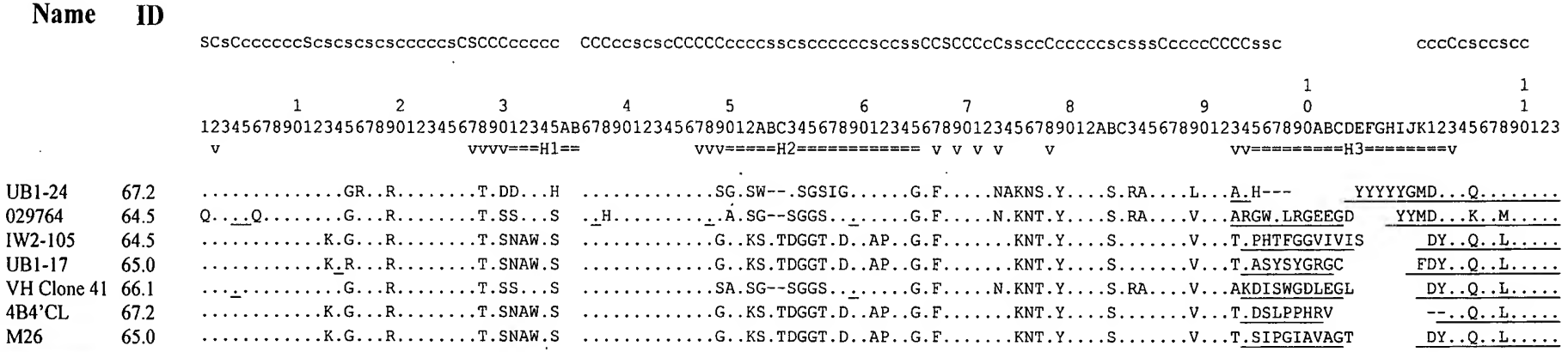


Figure 17B

Name	ID	All	Surface	Core	Kabat CDR	FR	FR Surface	Core FR	FR Near CDR	Vernier	V_H	J Chain	Closest Human Germline Gene	H1 Size	H2 Size	H3 Size	H1 Class	H2 Class
1D9 V_H	100.0	117	29	84	30	87	21	65	30	16	100	17		5	19	6	1	4
030094	67.7	86	19	67	15	72	17	57	26	12	75	13	DP-29-122+	Same	Same	16	Same	Same
N51P8	68.3	86	18	66	15	72	16	57	25	12	75	13	DP-29-122+	Same	Same	15	?	Same
IW2-91	67.5	85	18	65	15	72	16	56	25	12	75	12	DP-29-122+	Same	Same	15	Same	Same
H2-46	66.7	84	18	65	15	72	16	56	25	12	75	12	DP-29-122+	Same	Same	15	Same	Same
039158	72.2	83	17	64	15	71	15	56	25	12	74	12	DP-29-122+					
038064	65.6	82	17	64	14	71	15	56	25	11	74	12	VH26Rabbitts+					
038062	64.6	82	17	63	14	71	15	56	25	11	73	12	VH26Rabbitts+					
32.B9	64.6	82	17	63	14	71	15	56	25	11	72	12	VH26Rabbitts+	Same	17	19	Same	3
038062	64.6	82	17	63	14	71	15	56	25	11	72	12	VH26Rabbitts+					
034514	69.8	81	17	63	14	70	15	56	25	11	72	12	VH26Rabbitts+					
038066	65.3	81	16	63	14	70	15	55	25	11	71	12	VH26Rabbitts+					
035365	65.9	81	16	63	14	70	15	55	25	11	71	12	VH26Rabbitts+					

Figure 18A

Name	ID	All	Surface	Core	Kabat CDR	FR	FR Surface	Core FR	FR Near CDR	Vernier	V_H	J Chain	Closest Human Germline Gene	H1 Size	H2 Size	H3 Size	H1 Class	H2 Class
Hb-5	69.2	81	16	63	14	69	15	55	25	11	71	12	VH26Rabbitts+					
4G12	64.8	81	16	63	14	69	15	55	25	11	71	12	VH26Rabbitts+	Same	17	16	Same	3
VH clone 39	66.7	80	16	63	14	69	14	55	25	11	71	12	VH26Rabbitts+	Same	17	11	Same	3
040094	62.5	80	16	63	14	69	14	55	25	11	71	12	LSG3.1					
VH clone 18	63.0	80	16	63	13	69	14	55	25	11	71	12	VH26Rabbitts+	Same	17	18	Same	3
UB1-24	67.2	80	16	63	13	69	14	55	25	11	71	12	DP-31-V39P+	Same	17	10	Same	3
029764	64.5	80	16	63	13	69	14	55	25	11	71	12	VH26Rabbitts+	Same	17	15	Same	3
IW2-105	64.5	80	16	63	13	69	14	55	25	11	71	12	LSG3.1	Same	Same	13	Same	?
UB1-17	65.0	80	16	63	13	69	14	55	25	11	71	11	LSG3.1	Same	Same	12	Same	?
VH clone 41	66.1	80	16	62	13	69	14	55	25	11	71	11	VH26Rabbitts+	Same	17	12	Same	3
4B4'CL	67.2	80	16	62	13	68	14	55	25	11	71	11	LSG3.1	Same	Same	8	Same	?
M26	65.0	80	16	62	13	68	14	55	25	11	71	11	LSG3.1	Same	Same	12	Same	?

Figure 18B

Kabat	#	FR or CDR	Mouse 1D9 V_K	Mouse κ-II		Human κ-II	Human Acceptor HF-21/28 (005056)	Surface or Core		1D9 RK_A	1D9 RK_B	Comment
1	1	FR1	D	D*		D		S		D	D	
2	2		V	V		I*		C		V	V	
3	3		V	V		V*		S		V	V	
4	4		M	M		M		C		M	M	
5	5		T	T*		T		C		T	T	
6	6		Q	Q*		Q		C		Q	Q	
7	7		T	T		S	S	S		S	S	
8	8		P	P		P		c		P	P	
9	9		L	L		L		s		L	L	
10	10		T	S		S	S	C		S	S	
11	11		L	L		L*		c		L	L	
12	12		S	P		P	P	c		P	P	
13	13		V	V*		V*		c		V	V	
14	14		T	S		T		c		T	T	
15	15		V	L		P	L	s		L	L	
16	16		G	G		G		c		G	G	
17	17		H	D		E	Q	c		Q	Q	
18	18		P	Q		P		s		P	P	
19	19		A	A		A		c		A	A	
20	20		S	S*		S		c		S	S	
21	21		I	I*		I		c		I	T	
22	22		S	S*		S*		C		S	S	
23	23	FR1	L	C		C		C		C	C	
24	24	CDR1	K	R		R	R	s		K	K	
25	25	|	S	S*		S*		c		S	S	
26	26	|	S	S*		S		s		S	S	
27	27	|	Q	Q		Q		s		Q	Q	
27A	28	|	S	S		S		s		S	S	
27B	29	|	L	L		L		c		L	L	
27C	30	|	L	V		L	V	s		L	L	
27D	31		Q	H		H	H	c		D	D	
27E	32	|	S	S		S		s		S	S	
27F			-			x				-	-	
28	33		D	N		D		s		D	D	
29	34	|	G	G*		G		c		G	G	
30	35	|	K	N		N	N	c		K	K	
31	36		T	T		N		c		T	T	
32	37	|	L	Y*		Y	Y	c		F	F	
33	38	|	L	L*		L		c		L	L	
34	39	CDR1	N	E		N		c		N	N	
35	40	FR2	W	W		W		C		W	W	
36	41		L	Y		Y	F	C		F	L	Δ1

Figure 19A

Kabat	#	FR or CDR	Mouse 1D9 V_K	Mouse κ-II		Human κ-II	Human Acceptor HF-21/28 (005056)	Surface or Core		1D9 RK_A	1D9 RK_B	Comment
37	42		L	L		L	Q	c		Q	L	Δ2
38	43		Q	Q*		Q		c		Q	D	
39	44		R	K		K		c		R	R	
40	45		P	P*		P		s		P	P	
41	46		G	G*		G		s		G	G	
42	47		Q	Q		Q		c		Q	Q	
43	48		S	S*		S		c		S	S	
44	49	|	P	P*		P		C		P	P	
45	50		K	K		Q	R	c		R	R	
46	51		R	L		L		C		R	R	
47	52		L	L*		L		C		L	F	
48	53		I	I*		I		C		I	I	
49	54	FR2	Y	Y		Y		C		Y	Y	
50	55	**CDR2**	L	K		L		c		**L**	**L**	
51	56	|	V	V		V	K	c		**V**	**V**	
52	57	|	S	S		S		c		**S**	**S**	
53	58	|	K	N		N		c		**K**	**K**	
54	59	|	L	R		R	N	c		**L**	**L**	
55	60	|	D	F		A	R	c		**D**	**D**	
56	61	**CDR2**	S	S*		S		s		**S**	**S**	
57	62	FR3	G	G		G		S		G	G	
58	63		V	V		V		C		V	V	
59	64		P	P		P		C		P	P	
60	65		D	D*		D		S		D	D	
61	66		R	R		R		C		R	R	
62	67		F	F*		F		C		F	F	
63	68		T	S		S	S	C		S	S	
64	69		G	G*		G		C		G	G	
65	70		S	S*		S		C		S	S	
66	71		G	G*		G		C		G	G	
67	72		S	S*		S		s		S	S	
68	73		G	G*		G		C		G	G	
69	74		T	T*		T		C		I	T	
70	75		D	D*		D		C		D	D	
71	76		F	F*		F		C		F	F	
72	77		T	T*		T		c		T	T	
73	78		L	L		C		c		L	L	
74	79		K	K		K		c		K	K	
75	80		I	I		T		c		I	I	
76	81		S	S		S		c		S	S	
77	82		R	R*		R		s		R	R	
78	83		V	V		V		c		V	V	
79	84		E	E		E		s		E	E	
80	85		A	A*		A		c		A	A	
81	86		E	E*		E		s		E	E	
82	87		D	D*		D		c		D	D	
83	88		L	L		V	V	c		V	V	
84	89		G	G*		G		c		G	G	
85	90		V	V		V		c		V	V	
86	91		Y	Y*		Y		c		Y	Y	
87	92		Y	Y		Y		C		Y	Y	
88	93	FR3	C	C		C		C		C	C	

Figure 19B

Kabat	#	FR or CDR	Mouse 1D9 V_K	Mouse κ-II		Human κ-II	Human Acceptor HF-21/28 (005056)	Surface or Core		1D9 RK_A	1D9 RK_B	Comment
89	94	CDR3	W	F		M		c		W	W	
90	95	|	Q	Q*		Q	M	c		Q	Q	
91	96	|	G	G		A		c		G	G	
92	97	|	T	T		L		c		T	T	
93	98	|	H	H		Q		c		H	H	
94	99	|	F	V		x		s		F	F	
95	100	|	P	P*		P	W	c		F	P	
95A		|	-	P		R				-	-	
95B		|	-	-		-				-	-	
95C		|	-	-		-				-	-	
95D		|	-	-		-				-	-	
95E		|	-	-		-				-	-	
95F		|	-	-		-				-	-	
96	101	|	Y	Y		x	-	c		Y	Y	
97	102	CDR3	T	T*		T	F	c		T	T	
98	103	FR4	F	F*		F		C		F	F	
99	104		G	G		G		c		G	G	
100	105		G	G		Q	Q	c		Q	G	
101	100		G	G		G		c		G	G	
102	106		T	T		T		c		T	T	
103	107		K	K*		K	R	s		R	R	
104	108		L	L		V		c		L	E	
105	109		E	E		E		s		E	E	
106	110		I	I		I		s		I	I	
106A			-	-		-				-	-	
107	111	FR4	K	K*		K	-	s		K	K	

Figure 19C

Kabat	#	FR or CDR	Mouse 1D9 V_H	Mouse IIIc		Human III	Human Acceptor 4B4'CL (000490)	Surface Or Core		1D9 RH_A	1D9 RH_B	Comment
1	1	FR1	L	E*		E		s		E	F	
2	2		V	V		V		C		V	V	
3	3		Q	K*		Q		s		Q	Q	
4	4		L	L*		L*		C		L	L	
5	5		V	E		V		s		V	V	
6	6		L	E		L		c		E	E	
7	7		S	S		S*		c		S	S	
8	8		G	G		G*		c		G	G	
9	9		G	G		G*		c		G	G	
10	10		G	G*		G		c		G	G	
11	11		L	L		L		S		L	L	
12	12		V	V*		V		c		V	V	
13	13		Q	Q		Q	K	s		K	K	
14	14		P	P		P*		c		P	P	
15	15		K	G		G*	G	s		G	G	
16	16		G	G		G		s		G	G	
17	17		S	S		S*		c		S	S	
18	18		L	M*		L*		c		L	L	
19	19		K	K*		R	R	c		R	R	
20	20		L	E		L		c		L	L	
21	21		S	S		S*		c		S	S	
22	22		L	C		C*		C		G	C	
23	23		A	V		A		c		A	A	
24	24		A	A		A		C		A	A	
25	25		S	S		S*		c		S	S	
26	26		G	G		G		c		G	G	
27	27		F	F		F*		C		F	E	
28	28		S	T*		T	T	C		T	S	Δ1
29	29		F	F*		F		C		F	F	
30	30	FR1	N	S		S	S	S		S	N	Δ2
31	31	CDR1	A	N		S	N	c		A	A	
32	32		Y	Y		Y	A	S		Y	Y	
33	33		A	T		A	W	S		A	A	
34	34		M	M		M		c		M	M	
35	35		N	N		S	S	c		N	N	
35a			-	-		-		c		-	-	
35b		CDR1	-	-		-		c		-	-	

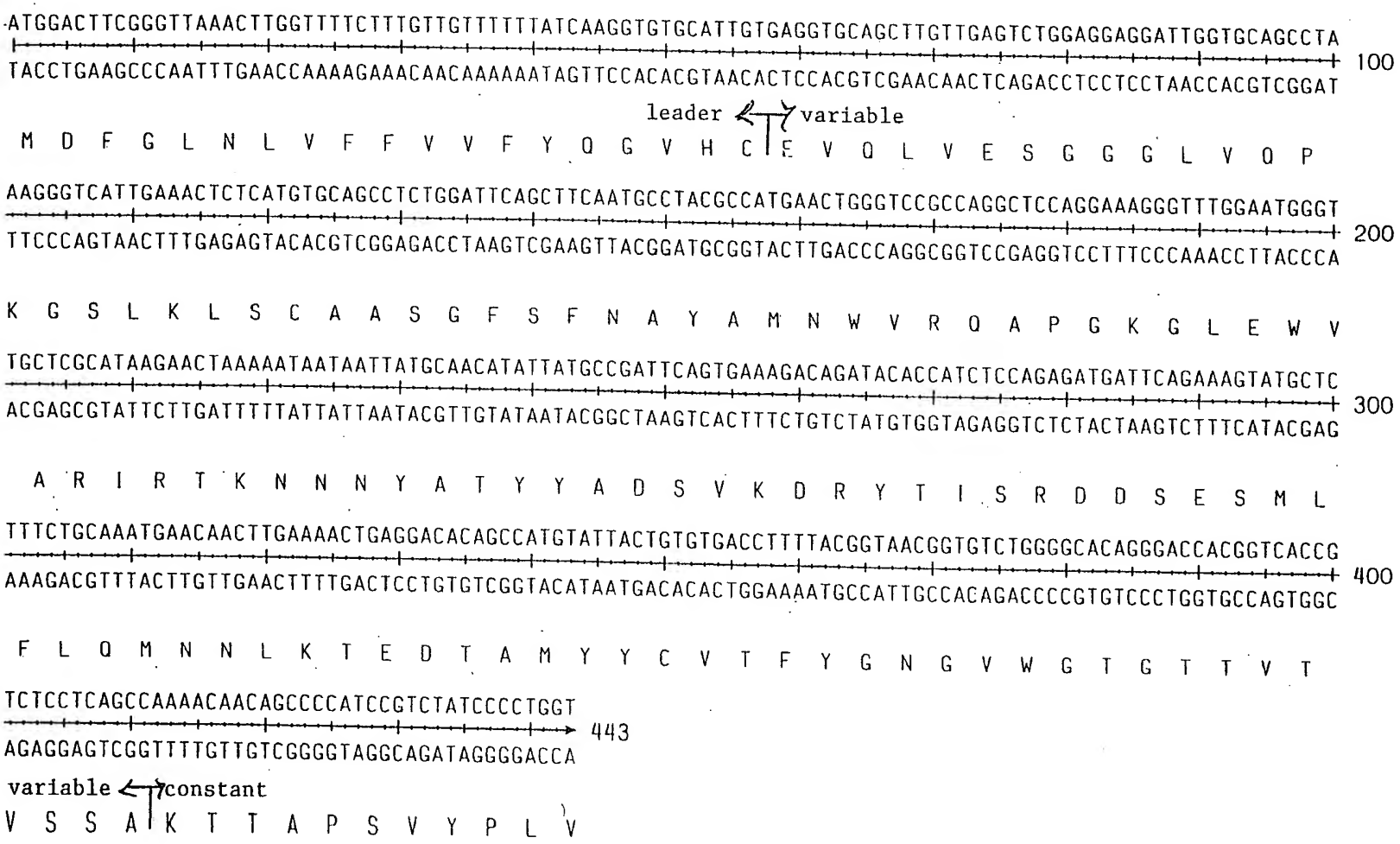
Figure 20A

Kabat	#	FR or CDR	Mouse 1D9 V_H	Mouse IIIc	Human III	Human Acceptor 4B4'CL (000490)	Surface Or Core	1D9 RH_A	1D9 RH_B	Comment
36	36	FR2	W	W	W*		C	W	W	
37	37	|	V	V	V*		C	V	V	
38	38	|	R	R	R*		C	R	R	
39	39	|	Q	Q	Q*		c	Q	Q	
40	40	|	A	S	A		c	A	A	
41	41	|	P	P	P		s	P	P	
42	42	|	G	E	G*		s	G	G	
43	43	|	K	K	K		s	K	K	
44	44	|	G	G	G		c	G	G	
45	45	|	L	L	L*		C	L	L	
46	46	|	E	E*	E		C	E	E	
47	47	|	W	W	W*		C	W	W	
48	48	|	V	V*	V*		C	V	V	
49	49	FR2	A	A	S	G	C	G	G	
50	50	**CDR2**	R	E	V		c	**R**	**R**	
51	51	|	**I**	I	I		c	**I**	**I**	
52	52	|	**R**	R	S	K	s	**R**	**R**	
52a	53	|	**I**	L	G	S	s	**T**	**T**	
52b	54	|	**K**	K	K*		s	**K**	**K**	
52c	55	|	**N**	S	T	T	c	**N**	**N**	
53	56	|	**N**	H	D	D		**N**	**N**	
54	57	|	**N**	N	G	G		**N**	**N**	
55	58	|	**Y**	Y	G	G		**Y**	**Y**	
56	59	|	**A**	A	S	T	s	**A**	**A**	
57	60	|	T	T	T		c	**T**	T	
58	61	|	**Y**	H	Y	D	c	**Y**	**Y**	
59	62	|	**Y**	Y	Y		c	**Y**	**Y**	
60	63	|	**A**	A	A		c	**A**	**A**	
61	64	|	**D**	E	D	A	s	**D**	**D**	
62	65	|	**S**	S	S	P	s	**S**	**S**	
63	66	|	V	V	V*		c	V	**V**	
64	67	|	**K**	K	K		s	**K**	**K**	
65	68	**CDR2**	**R**	G	G*	G	s	**D**	**D**	
66	69	FR3	R	R	R*		C	R	R	
67	70	|	Y	F	F*	F	C	F	F	
68	71	|	T	T	T		C	T	T	
69	72	|	I	I*	I*		C	**I**	I	
70	73	|	S	S	S*		S	S	S	
71	74	|	R	R	R*		C	**R**	R	
72	75	|	D	D	D		c	D	D	
73	76	|	D	D	N		C	D	D	
74	77	|	S	S	S		s	S	S	
75	78	|	E	K	K	K	s	K	K	
76	79	|	S	S	N	N	s	N	N	
77	80	|	M	S	T	T	c	T	T	
78	81	|	L	V	L		C	L	L	
79	82	|	F	Y	Y	Y	c	Y	Y	
80	83	|	L	L	L*		c	L	L	

Figure 20B

Kabat	#	FR or CDR	Mouse 1D9 V_H	Mouse IIIc		Human III	Human Acceptor 4B4'CL (000490)	Surface Or Core		1D9 RH_A	1D9 RH_B	Comment
81	84		Q	Q*		Q		c		Q	Q	
82	85		M	M		M*		C		M	M	
82a	86		N	N		N		s		N	N	
82b	87		N	N		S	S	s		S	S	
82c	88		L	L		L*		c		L	L	
83	89		K	R		R		s		K	K	
84	90		T	A		A		c		T	T	
85	91		E	E		E		s		E	E	
86	92		D	D		D		C		D	D	
87	93		T	T		T		c		T	T	
88	94		A	G		A*		c		A	A	
89	95		M	T		V	V	c		V	V	
90	96		Y	Y		Y*		c		Y	Y	
91	97		Y	Y		Y*		C		Y	Y	
92	98		C	C*		C*		C		G	C	
93	99		V	T		A	T	C		T	T	
94	100	FR3	T	T		R		C		T	T	
95	101	**CDR3**	**F**	G		G	D	c		**F**	**F**	
96	102		**Y**	F		R	S	c		**Y**	Y	
97	103		**G**	-		x	L	s		**G**	**G**	
98	104		**N**	-		G	P	c		**N**	**N**	
99			-	-		x	P	c		-	-	
100			-	-		S	H	c		-	-	
100 a			-	-		L		C		-	-	
100 d			-	-		S		C		-	-	
100 c			-	-		G				-	-	
100 d			-	-		x				-	-	
100 e			-	-		Y				-	-	
100 f			-	-		Y				-	-	
100 g			-	-		Y				-	-	
100 h			-	-		Y				-	-	
100 I			-	-		H				-	-	
100 j			-	-		Y				-	-	
100 k			-	F		F		C		-	-	
101	105		**G**	A		D	P	C		**G**	**G**	
102	106	**CDR3**	**V**	Y		Y		C		**V**	**V**	
103	107	FR4	W	W		W*		C		W	W	
104	108		G	G		G*		C		G	G	
105	109		T	Q		Q	Q	S		Q	Q	
106	110		G	C		G*		C		G	G	
107	111		T	T		T*		C		T	T	
108	112		T	L		L	L	C		L	L	
109	113		V	V		V*		C		V	V	
110	114		T	T		T*		C		T	T	
111	115		V	V*		V*				**V**	V	
112	116		S	S		S*				S	S	
113	117	FR4	S	S		S*				S	S	

Figure 20C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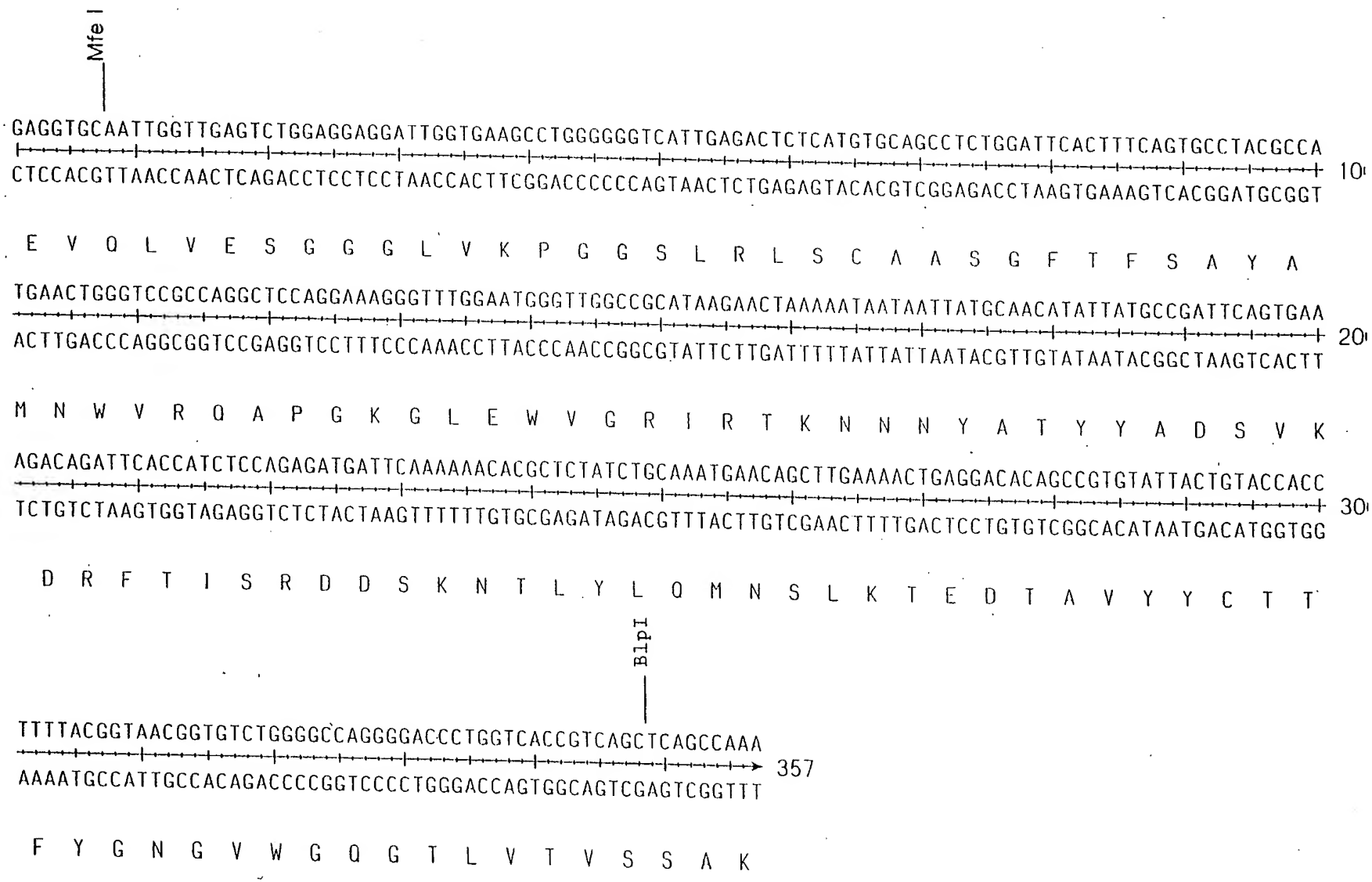
100
leader
variable
M D F G L N L V F F V V F Y Q G V H C E V Q L V E S G G G L V Q P
AAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTCAGCTTCAATGCCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGT
TTCCCAGTAACTTTGAGAGTACACGTCGGAGACCTAAGTCGAAGTTACGGATGCGGTACTTGACCCAGGCGGTCCGAGGTCCTTTCCCAAACCTTACCCA
200
K G S L K L S C A A S G F S F N A Y A M N W V R Q A P G K G L E W V
TGCTCGCATAAGAACTAAAAATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGATACACCATCTCCAGAGATGATTCAGAAAGTATGCTC
ACGAGCGTATTCTTGATTTTTATTATTAATACGTTGTATAATACGGCTAAGTCACTTTCTGTCTATGTGGTAGAGGTCTCTACTAAGTCTTTCATACGAG
300
A R I R T K N N N Y A T Y Y A D S V K D R Y T I S R D D S E S M L
TTTCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGACCTTTTACGGTAACGGTGTCTGGGGCACAGGGACCACGGTCACCG
AAAGACGTTTACTTGTTGAACTTTTGACTCCTGTGTCGGTACATAATGACACACTGGAAAATGCCATTGCCACAGACCCCGTGTCCCTGGTGCCAGTGGC
400
F L Q M N N L K T E D T A M Y Y C V T F Y G N G V W G T G T T V T
TCTCCTCAGCCAAAACAACAGCCCCATCCGTCTATCCCCTGGT
AGAGGAGTCGGTTTTGTTGTCGGGGTAGGCAGATAGGGGACCA
443
variable
constant
V S S A K T T A P S V Y P L V

Figure 21

BglI
ATGAAGTTGCCTGTTAGGCTGTTGGTGCTCTGGATTCGGGAGACAATCGGCGATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCGTTGGAC
TACTTCAACGGACAATCCGACAACCACGAGACCTAAGCCCTCTGTTAGCCGCTACAACACTACTGGGTCTGAGGTGAGTGAAACAGCCAATGGCAACCTG
100
leader
variable
M K L P V R L L V L W I R E T I G D V V M T Q T P L T L S V T V G
ACCCAGCCTCCATCTCTTGCAAGTCAAGAGCCTCTTAGATAGTGATGGAAAGACATTTTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAA
TGGGTCGGAGGTAGAGAACGTTCAGTTCAGTCTCGGAGAATCTATCACTACCTTTCTGTAAAAACTTAACCAACAATGTCTCCGGTCCGGTCAGAGGTTT
200
H P A S I S C K S S Q S L L D S D G K T F L N W L L Q R P G Q S P K
GCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTG
CGCGGATTAGATAGACCACACAGATTTGACCTGAGACCTCAGGGACTGTCCAAGTGACCGTCACCTAGTCCCTGTCTAAAGTGTGACTTTTAGTCGTCTCAC
300
R L I Y L V S K L D S G V P D R F T G S G S G T D F T L K I S R V
GAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTG
CTCCGACTCCTAAACCCTCAAATAATAACGACCGTTCCATGTGTAAAAGGCATGTGCAAGCCTCCCCCCTGGTTCGACCTTTATTTTGCCCGACTACGAC
400
variable
constant
E A E D L G V Y Y C W Q G T H F P Y T F G G G T K L E I K R A D A
CACCAACTGTATCCATCTTCCCACCA
426
GTGGTTGACATAGGTAGAAGGGTGGT
A P T V S I F P P

Figure 22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10
E V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S A Y A
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ACTTGACCCAGGCGGTCCGAGGTCCTTTCCCAAACCTTACCCAACCGGCGTATTCTTGATTTTTATTATTAATACGTTGTATAATACGGCTAAGTCACTT
20
M N W V R Q A P G K G L E W V G R I R T K N N N Y A T Y Y A D S V K
AGACAGATTCACCATCTCCAGAGATGATTCAAAAAACACGCTCTATCTGCAAATGAACAGCTTGAAAACTGAGGACACAGCCGTGTATTACTGTACCACC
TCTGTCTAAGTGGTAGAGGTCTCTACTAAGTTTTTTGTGCGAGATAGACGTTTACTTGTCGAACTTTTGACTCCTGTGTCGGCACATAATGACATGGTGG
30
D R F T I S R D D S K N T L Y L Q M N S L K T E D T A V Y Y C T T
BlpI
TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCTGGTCACCGTCAGCTCAGCCAAA
AAAATGCCATTGCCACAGACCCCGGTCCCCTGGGACCAGTGGCAGTCGAGTCGGTTT
357
F Y G N G V W G Q G T L V T V S S A K

Figure 23

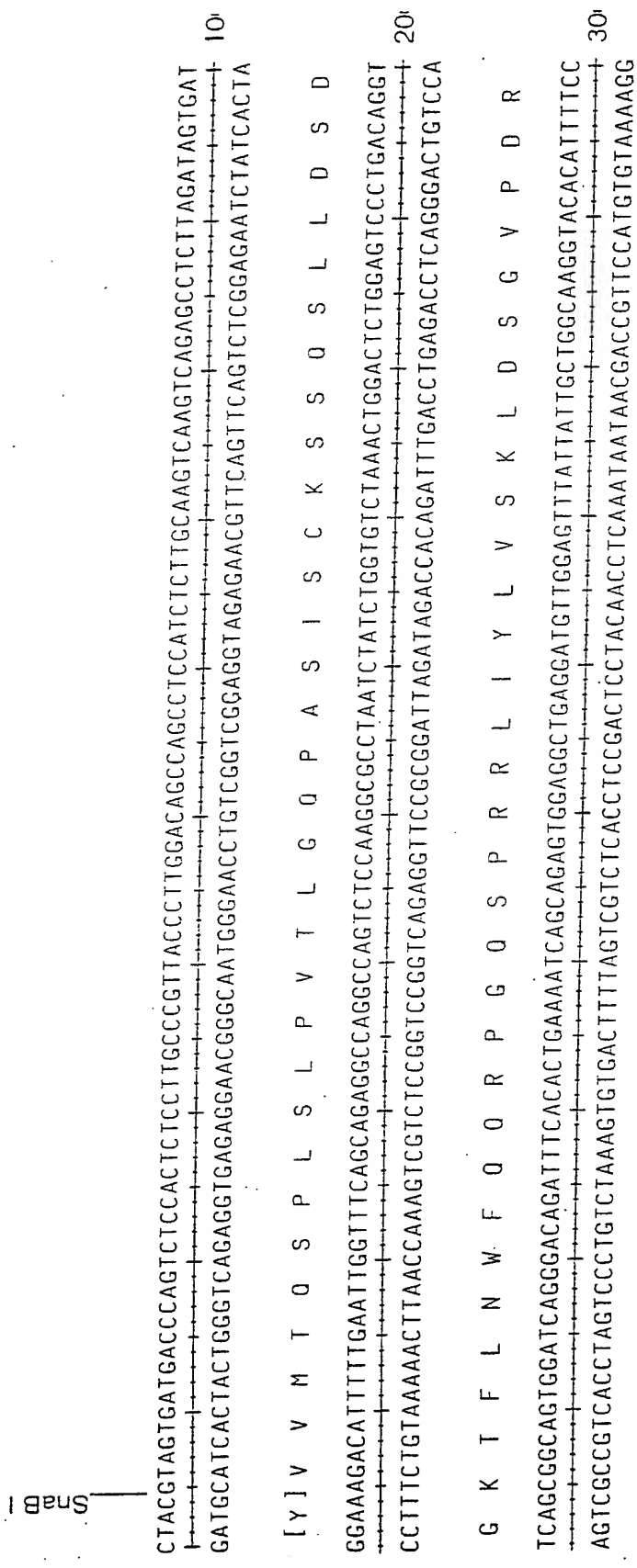
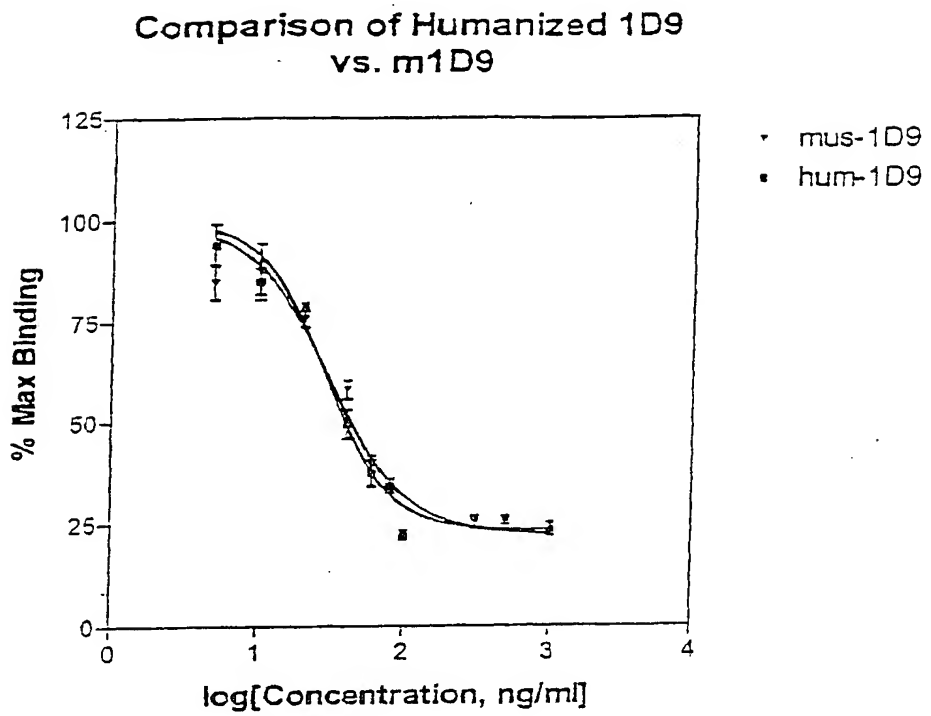

SnaB I
BsiWI
10'
20'
30'
3'
[Y] V V M T Q S P L S L P V T L G Q P A S I S C K S S Q S L L D S D
G K T F L N W F Q Q R P G Q S P R R L I Y L V S K L D S G V P D R
F S G S G S G T D F T L K I S R V E A E D V G V Y Y C W Q G T H F P
Y T F G Q G T R L E I K R T

Figure 24



	hum-1D9	mus-1D9
Equation 1		
Best-fit values		
BOTTOM	23.46	22.40
TOP (Constant)	100.0	100.0
LOGEC50	1.452	1.472
HILLSLOPE	-1.972	-1.627
EC50	28.32	29.68
Std. Error		
BOTTOM	2.656	3.945
LOGEC50	0.04151	0.06251
HILLSLOPE	0.2946	0.3143
95% Confidence Intervals		
BOTTOM	17.18 to 29.74	13.07 to 31.73
LOGEC50	1.354 to 1.550	1.325 to 1.620
HILLSLOPE	-2.668 to -1.275	-2.370 to -0.8835
EC50	22.59 to 35.51	21.12 to 41.71
Goodness of Fit		
Degrees of Freedom	7	7
R squared	0.9931	0.9858
Absolute Sum of Squares	48.60	88.53
Sy.x	2.635	3.556
Data		
Number of X values	10	10
# of Y replicates (mean analyzed)	3	3
Total number of values	10	10
Number of missing values	20	20

Figure 25